STIC-Biotech/ChemLib

. Ce 0964

From:

Bunner, Bridget

Sent: To: Monday, February 25, 2002 12:20 PM STIC-Biotech/ChemLib

To: Subject:

sequence search

Hi! I'd like a sequence search performed for case 09/755,017:

1. the nucleic acid sequence of SEQ ID NO: 1

2. the nucleic acid sequence that encodes the amino acid sequence of SEQ ID NO: 2

thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 305-7148 mailroom 10C01

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 JEOT TEL: 308-3534

TYPE OF SEARCH:

NA Sequences: 2

AA Sequences: Structures: Struct

VENDOR/COST(where applic.)
STN: _____
DIALOG: ____
Questel/Orbit: ____
DRLink: ____
Lexis/Nexis: ___
Sequence Sys.: ____
WWW/Internet: ____
Other (specify):

CM1 PRI 1911 Suc Spart

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Title:
Perfect score:
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Maximum DB
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AZ511623 1M0356C17
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BH111304 RPCI-14-3
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• source	SEATINES.	***	• 1.x°	(5, 4)	(₄)	: ""	. 7	٠ ,	COMMENT	į., JOURNAL		TITLE	*	: 14	AUTHORS	REFERENCE			: ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AQ077154/c	RESULT 1
1. 479 /organism="Homo sapiens"	Class: BAC ends.	<pre>http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. seq primer: M13-21</pre>	Clones are available from Research Genetics (info@resgen.com). BAC end search page:	Fax: 301 838 0208 Email: mdadams@tigr.org	Tel: 301 838 0200	The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA	Department of Eukaryotic Genomics	Contact: Mark Adams	Other_GSSs: CIT-HSP-2354D1.TR	Unpublished (1998)	Map Building	Use of a random human BAC End Sequence Database for Sequence-Ready	Venter, J.C.	Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,	1 (bases 1 to 479)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	GSS.	AQ077154.1 GI:3438338	AQ077154	CIT-HSP-2354D1.TF CIT-HSP Homo sapiens genomic clone 2354D1, DNA	AQ077154 479 bp DNA GSS 20-AUG-1998		

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KEYWORDS
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                           vv74c09.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1228144 3' similar to SW:OLF2_HUMAN Q15062 OLFACTORY RECEPTOR-LIKE PROTEIN FAT11. ;, mRNA sequence.
                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                  Email: mouseest@watson.wustl.edu
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/note-"organ: skin; Vector: pBluescript SK-; Site_1:
/note-"organ: skin; Vector: pBluescript SK-; Site_1:
/note-"organ: skin; Vector: pBluescript SK-; Site_1:
/note-"organ: skin; Vector: primer: Ol
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP xR Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3'-3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
a 133 c 150 g 89 t 2 others
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1228144"
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TGA---ACCACTTCTTCTGAGATGCTTGTTCTCCTGAAGCTGGCTTGTGAGGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 27 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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The Institute for Genomic Research
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Other_GSSs: RPCI-23-27B20.TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                   Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000)
                                 FANTOM Consortium. Functional annotation of a Nature 409, 685-690 (2001)
                                                                                                 The
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
                    Nature 409,
5 (bases 1
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Carninci, P., Shibata, Y.,
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Akahira,S.,

Akimura, T.,

Aono, H.,

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Saisaski, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
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Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sal 3' end: BamHI. Host: DH10B.
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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VYTMHFPFCMSQBIRHLLCEVPPLLKLACADTSQYELMYVVTGVIFLLLPLSAIITSY
SLILFTVLHMPSNEGRKKALVTCSSHLTVVGMFYGGATFMYVLPSSFHSPKQDNIISV
FYTIVTPALNPLIYSLRNKEVIGAVRRVLGRHILPAHATV"

337 c 304 g 398 t
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/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/LIGHTSTAND"
LLLVITVDARLHVPMYLLLRQLSLIDLLFTSVVTPNTVVDFILLRUTTSFEGGLALGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/db_xref="MGD:MGI:1894709"
/db_xref="MGD:MGI:1914036"
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Hayatsu, N.,

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                                                             1 (bases 1 to 3063)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                       AK016560.1
CAP trapper
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itch,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata, K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogaba,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
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RIKEN Genome Exploration Research Group Phase II Team and
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                                                                                                                                                /db_xref="taxon:10090"
/db_xref="MGD:MGI:1907565"
/db_xref="MGD:MGI:1921647"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                 /sex="male"
                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
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                                           703 caaaaagcatttgggacatgtggttcccatctaattgtggtgtctcttttttatagtaca
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VYTMHFPFCMSQEIRHLLCEVPPLLKLACADTSQYELMVYVTGVIFLLLPLSAIITSY
SLILFTVLHMPSNEGRKKALVTCSSHLTVVGMFYGGATFMYVLPSSFHSPKQDNIISV
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438. .1388
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/db_xref="GI:12855358"
/translation="WepPunSTLESGFILVGILDGSGSDELLCATVTTLYMLALISNGL
/LLVITVDARLHVPMYLLLRQLSLIDLLFTSVVTPNTVVDFLLRDNTISFEGCALQLF
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612 c 696
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GCCACTTTCATGTATGTGCTGCCCAGTTCCTTCCACAGTCCTAAGCAAGACAATATCATC 1259

gccgtctctgtgtacctgcaaccaccttcgcccagctccaaggaccaaggaaaagatggtt

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2M0241J24R Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M0241J24 R, DNA sequence.
AZ969227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0241 row: J column: 24
Seg primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers
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Location/Qualifiers
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                                                                                                  10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from m. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0241J24"
                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
              selected for ampicillin resistance. 166 c 129 g 217 t
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Query Match
Best Local Similarity
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                                                       Unpublished (2000)
Contact: Robert B.
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Mammalia; Eutheria;
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1M0356C17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0356C17 R, DNA sequence.
                 University of Utah University of Utah
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Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                          642
                                                                                                                                                                                                                                                                                                                                                                   441 CAATGAAGTGCAGATGTCCATAGCCAGTGTTATCCTCCTAGTGTTACCCCTTGGCCATTAT 382
                                                                                                                                                                                                                                                                                                                                                                                                       582 aaatgaggetgaaetatteettgteagtgagetetteeatetaataeeeetgaeaeteat 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 AGATAACATTGTGTGTGAAGTTCCAGCCCTGATTCAGCTGTCCAGTGCAGATACTACCTA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 tatcatgcaccagagactctgcctccagttggcagccgcatcctgggttactggttttag 461
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les 313; Conserv
AGTAACAGGTGTCTATCTTCAACCCAAGACTCACTATGCTCATGAATGGGGAAAGTTTCT
                                                      agoogtototgtgtacotgcaaccaccttcgcocagctccaaggaccaaggaaagatggt 821
                                                                                                                                                         acaaaaagcatttgggacatgtggttcccatctaattgtggtgtctcttttttatagtac 761
                                                                                                                                                                                                                                             CCTTTCCTCCTATGGTGCTATTGTGAAATCTGTTTTGAAGATAAAGTCACCTGCAGGGCA 322
                                                                                                                                                                                                                                                                                ccttatatcatatgcttttattgtccgagcagtattgaggatacagtctgctgaaggtcg 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agatcactttctctgtgaagtccctgcactgctcaagttatcttgtgttgagacaacagc 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGTCTCTGATCCAATCTACTGCTACCCTCAGGTTGCCCCTTTTGCTCTCAGCGGGTAGT
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Insert Length: 10000 Std Error: |
Plate: 0356 row: C column: 17
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
127 c 141 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0356C17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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'note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%;
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Pred. No. 1.5e-43;
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                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACACTTTTCTACACTGTAATAACTCCAACTCTTAACCCTCTCATTTATACACTGAAGAA 142
                                                                    AAAGTACAGCCGTCTCTGTGTACCTGCAACCACCTTNGCCCAGCTCCAAGGACCAAGGAA 269
                                                                                                                                        186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N68399 428 bp mRNA EST 13-MAR-1996 zal3b04.sl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 292399 3' similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., I
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E.,
,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N68399.1 GI:1224560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
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                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 428)
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314 286 1810
                                                                                                                                        Conservative
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                                                                                                                                                                                                                                           constructed by Bento Soares and M.Fatima Bonaldo."
90 c 90 g 128 t 1 others
                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GDB:3800175"
/db_xref="taxon:9606"
/clone="IMAGE:292399"
                                                                                                                                                                                                                                                                                                                 (Pharmacia),
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens
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                                                                                                                                                                                                                                                                              Eco RI sites of the modified pT7T3 vector. It through one round of normalization. Library
                                                                                                                                                       19.78;
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Primates;
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Pred. No. 4e-4
0; Mismatches
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                                                                                                                                         759 tacagccgtctctgtgtacctgcaaccaccttcgcccagctccaaggaccaaggaaagat
                                                                                                                                                                                                   Local Similarity 100 nes 184; Conservative
                                                                                                                           _
gaacaaggaggtaaaggaaggctttaaaaggttggttgcaagagtcttcttaatcaagaa
                                                                   TACAGCCGTCTCTGTACCTGCAACCACCTTCGCCCAGCTCCAAGGACCAAGGAAAGAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11010 Torreyana Road,
Tel: 8584048436
Fax: 8584046719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aurora Biosciences Corp.
Aurora Biosciences Corp.
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AST-2HBG3005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Greg Henkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exon-trap tags from a HL-60 GenomeScreen(TM) Library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henkel,G., Liyanage,M., Pratt,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 326)
                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                   /note="Organ: peripheral blood; vector: pAmp-1; 3' RACE total RNA from genetrap pools; shotgun clone in pAmp-1 used to transform DH5-alpha competent bacteria."

65 c 57 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="promyeloblast"
/cell_line="HL-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="acute promyelocytic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Genetrap HL-60 Human Promyelocytic
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5 Genetrap HL-60 I
s genomic 5', DNA
                                                                                                                                                                                                                       19.5%;
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                                                                                                                                                                                                                   Score 184; DB 13;
Pred. No. 9.1e-41;
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                                                                                                                                                                                                                                       Length 326;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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223 acatgtacagtcccacaaatgctagtaaatttatgcagcatcaggaaagtaatcagttat 282
                                                                                                                                                                      103
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                                                                           cttcatacccccatgtattttttttttttaccaatctatcactcctggatctttgttacacc 222
                                                                                                                                                            tacactgtgaccatctttggcaatctgaccattattctagtgtcacgcctggacaccaaa 162
                                                      CTGCACACCCCTATGTACTTCTTTCTTTCTCATCTGGCCATTCTTGACATATCCTATGCT 125
                                                                                                                              TACATCTTCAGCCTGCCCAAATGGAATAATCTTAGTAGTCATCTGCCTGGACCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html Plate: 367 row: N column: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvattsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH111304
RPCI-24-367N6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                            /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: Bar
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: Bar
RPCI-24 Mouse BAC Library produced by Pieter de Jor
library was cloned in the pTARBAC1 cloning vector
BamH1 sites using MboI partially digested male C5
                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="RPCI-24-367N6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism≖"Mus musculus"
/strain="C57BL/6J"
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Rodentia;
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                                                                                                                                                                                                    Score 180.4; DB 13; Length Pred. No. 1.2e-39; O; Mismatches 351; Indels
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Sciurognathi; Muridae;
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e RPCI-24-367N6,
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         Email: szhao@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                       BAC end sequences of library
Unpublished (1997)
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ516219 640 bp DNA
RPCI-11-350G23.TVK RPCI-11 Homo
RPCI-11-350G23, DNA sequence.
                                                                                                                               9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                    Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
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Mammalia; Eutheria;
1 (bases 1 to 640)
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Primates;
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Catarrhini; Hominidae
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1M0188F05F Mouse 10kb p

Clone UUGC1M0188F05 F, I

AZ413817

AZ413817.1 GI:10537830

GSS.
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                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duv
Islam,H., Longacre,S., Mahmoud,M., Meenen,E.,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., v
and Wright,D.,Weiss,R.
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                        Email: ddunn@genetics.utah
Insert Length: 10000 Std
Plate: 0188 row: F column
                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                         Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                                                                           Mouse whole genome plasmid inserts
                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                 Rm.
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Mammalia; Eutheria;
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                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Sex="Male"
/Sex="Male"
/Sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
RPCII1 Human Male BAC 216 t
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                                                                                                 Biomedical
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/clone="RPCI-11-350G23"
/clone_lib="RPCI-11"
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/db_xref="GDB:7634182"
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93.0%;
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Rodentia;
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F, DNA sequence.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGACTCTCAGCTCCATACTCCCATGTATTTCTTCTTATCTAATTTGTCTTTCGTGGAC 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttcttgatttcttacactgtgaccatctttggcaatctgaccattattctagtgtcacgc 150
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               AZ607393 740 bp DNA GSS 13-DEC-2000 IM0429N15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0429N15 R, DNA sequence.
AZ607393 AZ607393.1 GI:11729583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared; adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptored DNA was purified and size-selected for a 9.5 to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                  244 ctagtaaatttatgcagcatcaggaaagtaatcagttatcgtggctgtgtagcccagctt 303
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reill;
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A
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             276
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                  polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.
                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429N15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="mouse 10kb plasmid UUGC1M library"
/sex="Male"
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tttcttaccaatctatcactcctggatctttgttacaccacatgtacagtcccacaaatg 243

AATCTTGGAATGATCATTTTGATCAGAATGGATCCACAGCTTCACACACCAATGTACTTT 638

Conservative

0;

Mismatches 320;

1;

Gaps

18.3%; 53.9%;

Score 172; DB 13; Pred. No. 2.5e-37;

Length 740; Indels

CTTGTAGACCTACTGTCTAAGAATACATCTATTCCTTTTCTTGGCTGTGCTATGCAGTTC

518

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AZ271125/c
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                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ271125 548 bp I
RPCI-23-146J4.TV RPCI-23
                                                                                                                                                                                         9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-23-146J4.TJ
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                                                                                                                                                                                                                                                            Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                      Plate: 146
                                                                    http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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                     BAC ends
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Tsegaye,G., Geer,
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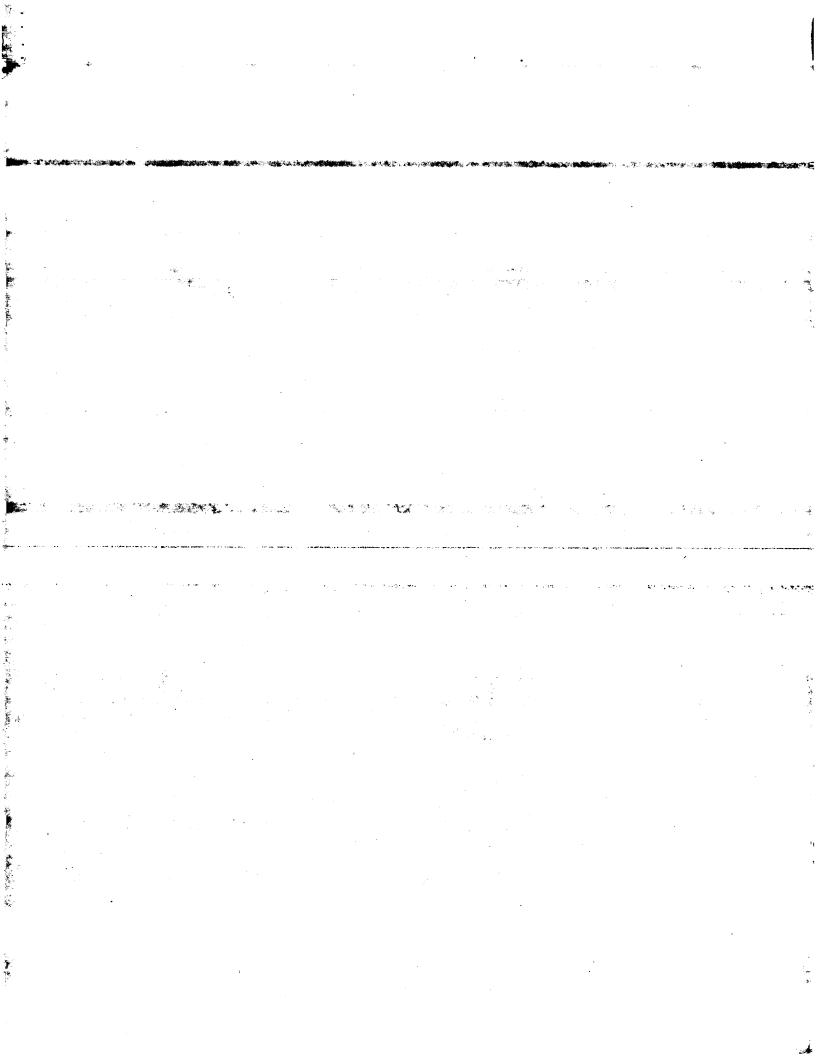
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260;
           plasmid inserts
Unpublished (2000)
                                                           Dunn, D., Aoyagi, A., Barber, M., Islam, H., Longacre, S., Mahmoud, M., Rose, M., Rose, R., Stokes, and Wright, D., Weiss, R.
                                                                                                                                                                                                                                         AZ765752 632 bp DNA GSS 1M056219R MOUSE 10kb plasmid UUGC1M library clone UUGC1M0562E19 R, DNA sequence.
                                                                                                                                                                                                            GSS
                                               Mouse whole genome
                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 632)
                                                                                                                                                                            Mus musculus
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                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                              house mouse.
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/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-146J4"
Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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Pred. No. 4.1e-35;
                                                                                            rber, M., Beacorn, T., Mahmoud, M., Meenen, E
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                                                                             R., Tingey, A.,
                                                                                            Meenen, E.,
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                                                   TCCTTGGATGGCTTCATGTTCACCCCTGTCACCATGACCTTCCCATTCTGTGGATCCCGG
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Insert Length: 10000 Std Error:
Plate: 0562 row: E column: 19
Seg primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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Rm. 308, Biomedical Polymers Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemically-competent E. coli XL10-Gold and selected for ampicillin resistance 195 c 129 g 184 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptored vector DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
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> g В Š. Ω, 8 당 δÕ g Ş 697 493 GTCATTTCAGGCTCCTATACATCCATCCTCCTCACTGTTCTCAGGATGAACTCAGCAGAG 637 373 612 GGTGCTGCTATCTATACCTAC 757 agtacagccgtctctgtgtac 433 TGGCTCTATGAGACCCTCATGTATGTGTGCTGTGTGCTCATGCTTCTCATCCCTGTGACA ggtcgacaaaaagcatttgggacatgtggttcccatctaattgtggtgtctcttttttat 756 ctcatccttatatcatatgcttttattgtccgagcagtattgaggatacagtctgctgaa 696 GAGATCCATCACTTCTTCTGTGAGGTCCCTGCTGTGACAAAGCTCTCCTGCTCAGACACC GGCCAGAAGAAGGCCCTTGCCACCTGCTCCT-CCACATGACTGTGGTCACCCTCTACTAT acagcaaatgaggctgaactattccttgtcagtgagctcttccatctaatacccctgaca 632 492 611 636 432 552

Search completed: February 26, 2002, 04:38:34 Job time: 3753 sec



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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL	ACCESSION VERSION KEYWORDS SOURCE ORGANII	H 0	RESULT	 .	45	4.4	: 41 42	ი ა 4	.c 37	u		·wu	. 30	228	26	25	23	. 21	20	_ بر د	c 16	15	c 13	11	. 10	o co ·	7 6	υ ≠		 2 P	Result
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396 ;; olfactory receptor; ribosomal protein; RPLP2. Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.) 00) Sanger Centre, Hinxton, Cambridgeshire, enquiries: humquery@sanger.ac.uk Clone	DNA PRI rom clone RP3-408B20 on ch Contains a gene and two p ptors (olfactory family) a OS acidic ribosomal protei		ALIGNMENTS	HSA302561	HSA302559	HSA302565 HSA302566	AC091612 AL357039	AL365336 AL390860	HSDJ31316	HS80I19 AC011571	HSA302545	HSA302543	HSA302541 HSA302542	HSA302540	HSA302538	~ 01	RATOL1RECE	U86275	U86270	AL589742 AL589651	AC024428 AC025941	HS193B12	HSA302591 HSA302592	HSA302590	HSA302588	HSA302586	HSA302585	HSA302593	AL133267 AC025941	ID	
	somal protein; RPLP rata; Euteleostomi;	25-OCT-2000 iromosome 6 Contains seudogenes for novel and a gene for a novel nd a gene for a novel n P2 (RPLP2),			Homo sa	Homo sa	Homo sa	AC091612 Homo sapi AL357039 Homo sapi	AL365336 Mus muscu Al390860 Human DNA	ALIZI944 Human DNA	AL022727 Human DNA AC011571 Homo sapi	AJ302545 Homo sapi	AJ302543 Homo sapi	AJ302541 Homo sapi	AJ302539 Homo sapi AJ302540 Homo sapi	AJ302538 Homo sapi	AJ302546 Homo sapi	AL589651 Mus muscu L34074 Rat OL1 rec	U86275 Homo sapien	U86270 Homo sapien	AL589742 Mus muscu	ACU24428 Homo sapi ACU25941 Homo sapi	298744 Human DNA's	AJ302591 Homo sapi AJ302592 Homo sapi	AJ302590 Homo sapi	AJ302588 Homo sapi	AJ302586 Homo sapi	AJ302585 Homo sapi	AJ302593 Homo sapi	AL133267 Human DNA AC025941 Homo sapi	Description

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RP3-408B20 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furthe details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RP3-408B20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-31316 is at 44689 in this sequence right end of clone RP1-193B12 is at 100 in this sequence.
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On Sep 18, 2000 this sequence version replaced gi:9588470.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        match: proteins: Tr:076000 Tr:076001 Tr:076002 Tr:035434
Sw:015062 Tr:099WD9 Sw:013607 Tr:099806 Tr:063394
Tr:099W13 Tr:095918 Tr:099U84 Tr:0990806 Tr:09Y3N9
Tr:0990212 Sw:095156 Sw:095157 Tr:09UGF6 Tr:09Y299
Tr:099UL5 Tr:062007 Sw:P23375 Tr:095371 Tr:09UJA0
Tr:090Z18 Tr:090Z19 Tr:09PSJ3 Tr:P70526 Tr:090Z21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (olfactory family) (h56M1-33P) pseudogene)
match: cDNAs: Em: M64392 Em: AF102516 Em: Y15524 Em: Y15525 Em: X88699 Em: AF1025251 Em: AF042016 Em: AF044033 Em: AF102525 Em: AF044034 Em: AF044035 Em: AF044037 Em: AF044035 Em: AF044037 Em: Y14442 Em: AF044037 Em: Y15529 Em: AF102529 Em: AF044038 Em: AF091557 Em: Y15529 Em: AF102529 Em: AF044038 Em: AF091553 Em: AF0440200 Em: M64391 Em: AF102532 Em: AF102533 Em: M64376 Em: AF091573 Em: AF091578 Em: AF0440385 Em: AF044033 Em: M64386 Em: M64388 Em: AF044038 Em: AF044038 Em: AF044038 Em: AF044038 Em: AF044038 Em: AF044038 Em: M64388 Em: AF044038 Em: AF044038 Em: M64388 Em: AF04408 Em: M64388 Em: AF044038 Em: M64388 Em: AF044038 Em: M64388 Em: 
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                         'note="AluJo repeat: matches 1.
                                                                                                                                                                                                              note="match: GSS: Em:AQ456128"
                                                                                                                                                                                                                                                                                                                  evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                               'pseudo
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                                                             2382
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copies
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ag 79% conserved"
                                                                                                         .280 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .301 of consensus"
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                                                                                                Sw:Q95156 Tr:Q9UGF4 Tr:Q9WU86 Tr:O60403
Sw:P37070 Tr:Q9QW38 Tr:O77758 Tr:Q9QZ17
Tr:Q9ROK4 Tr:O60412 Tr:Q9QY00 Tr:Q9QW36
                                                                                                                                                       match: ESTS: Em:N68399
match: proteins: Tr:Q43883 Tr:Q9QZ21 Tr:Q9Z1K0 Tr:Q9QZ20
Tr:Q63394 Tr:Q9Q499 Tr:Q9QZ19 Sw:P23270 Tr:Q9Y3P7
Tr:Q9QZ22 Tr:Q9Y299 Tr:Q62243 Tr:Q90807 Tr:Q90808
Tr:Q9WV13 Tr:Q63395 Tr:Q95918 Sw:P23266 Sw:P37069
                                                                               Sw:P37072 Sw:P37071 Tr:Q9Y3P5
                                                                                                                                                                                                                                                                                                                                                       /gene="dJ408B20.2"
20708. 21640
                                                                                                                                                                                                                                                           Em: AF034896
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/note="2 copies 46 mer 91% conserved"

complement(4227. .4576)

/note="match: STS: Em:G31214"
                                          /evidence=not_experimental
                                                                                                                                                                                                                                                                                Em: M64391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(15225
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complement(6590. 6889)
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complement(4834. .5686)
                                                                                                                                                                                                                                                                                                                                     /gene="dJ408B20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match:
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|6824. .17089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 58. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="AluJ/FLAM repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR16A repeat: matches 203. .307 of consensus" .0964. .11131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="HERVL repeat: matches 3244. .3919 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1P repeat: matches 900. .1509 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match: GSS: Em:U94441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSx repeat: matches 3. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluJb repeat: matches 29. 7090. .17158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note≖"MLT1H repeat: matches 1. .168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1P repeat:
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                                                                                                                                                                                                                                                                                Em: AF102540
dJ408B20.2 (novel 7 transmembrane receptor
family) (hS6M1-32))"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 580. .776 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                   repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS: Em:AQ544878'
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: G31213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Em: AQ100659*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 3813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: AQ100750'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Em: AQ748194"
                                                                                                                                                                                                                                                                            Em:AF044034 Em:Y14442 Em:X89700
3 Em:AF091573 Em:AF091574 Em:X89670
5 Em:AF010293 Em:M64388 Em:D12820
                                                                                                                                                                                                                                                                                                                                                                                                                   matches 5904. .6155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2750 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5344 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .311 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .81 of consensus"
                                                                                                Tr:076000
Tr:Q9R0K3
Tr:Q9UJA0
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgaattgggtaaatgacagcatcatacaggagtttattctgctgggtttctcagatcga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgcctccagttggcagccgcatcctgggttactggttttagtaactcagtgtggttgtct 480
                                                                                              gataggtttgtagctatttgtcggcctctccattactcagttatcatgcaccagagactc
                                                                                                                                                     CTTTTCATATTTCTGGCCTTGGGGGCTACTGAATATCTTCTCCTGGCCGTCATGTCCTTT
                                                                                                                                                                     cttttcatatttctggccttgggggctactgaatatcttctcctggccgtcatgtccttt
                                                                                                                                                                                                                                                atgctagtaaatttatgcagcatcaggaaagtaatcagttatcgtggctgtgtagcccag
                                                                                                                                                                                                                                                                                                   GGCAATCTGACCATTATTCTAGTGTCACGCCTGGACACCAAACTTCATACCCCCCATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                   ggcaatctgaccattattctagtgtcacgcctggacaccaaacttcatacccccatgtat 180
TGCCTCCAGTTGGCAGCTGCATCCTGGGTTACTGGTTTTAGTAACTCAGTGTGGTTGTCT
                                                                          GATAGGTTTGTAGCTATTTGTCGGCCTCTCCATTACTCAGTTATCATGCACCAGAGACTC
                                                                                                                                                                                                                            ATGCTAGTAAATTTATGCAGCATCAGGAAAGTAATCAGTTATCGTGGCTGTGTAGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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26069. .26126
/note="LiMB7 repeat: matches 61
26164. .26220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="FLAM_C repeat: matches 24448...24781
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TLTLQLPLCDPYVIDHFLCEVPALLKLSCVETTANEAELFLVSELFHLIPLTLILISY
AFIVRAVLRIQSAEGRQKAFGTCGSHLIVVSLFYSTAVSVYLQPPSPSSKDQGKMVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LTR15 repeat: matches 127.
complement(21244 . .21671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:B75689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNWVNDSIIQEFILLGFSDRPWLEFPLLVVFLISYTVTIFGNLT
IILVSRLDTKLHTPMYFFLTNLSLLDLCYTTCTVPQMLVNLCSIRKVISYRGCVAQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAC14158.1"
/db_xref="GI:10944516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSg/x repeat: matches 195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSq repeat: matches 1. .310 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%;
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Pred. No. 1.4e-258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 5206.
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Submitted (17-MAR-2000) Whitehead Institute/MIT

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                                             Grand-Pherre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McArim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T., M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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       Young, G., Zainoun, J., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                        Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHigh, W., Gage, D
                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome Unpublished
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Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG;
                                                                                                                                                                                                                                                                                       Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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FEATURES
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                                                           misc_feature
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On Apr 4, 2000 this sequence version replaced g1:72597
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                    110573 110572: conticution of the conticution of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 17827 bases at least 030 Consensus quality: 17827 bases at least 030 Consensus quality: 174151 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 4.5 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                 110673 131898: contig of
131899 131998: gap of
131999 176277: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 176000; agarose-fp insert size: 174877; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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2998 3097: gap of 100 bp
3098 5606: contig of 2509 bp in length
5607 5706: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0421 70520:
  /note="assembly_fragment'
3098. .5606
                                                        /clone="RP11-635011"
/clone_lib="RPCI-11 |
1. .2997
                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
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... gap of
37068: 7
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92325: contig of 11759 bp
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Younger,R.M., Amadou,C., Bethel,G., Ehler
Forbes,S.A., Horton,R., Milne,S., Mungall
Volz,A., Ziegler,A. and Beck,S.
Characterisation of clustered MHC-linked
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Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J., Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S
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Ehlers, A., Beck, S.,
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Younger,R.M. and Beck,S.
Polymorphisms in olfactory
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Springer-Verlag, Tok
2 (bases 1 to 1074)
                                                   MHC-linked olfactory receptor loci exhibit polymorphism contribute to extended HLA/OR-haplotypes
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iilvshydfklhtpmyfflsulslldlcyttstvpqmlvincntrkvisyggcvaqlf
iflalgsteclllavmcfdffvalcrplhysiimhqrlcfqlaaswiggfsusylqs
Twilkmplcghkevdhffcevpalkklscvdftaneaetffsvlflllstyaflkmplcghkevdhffcgshllvsltavaneaetffsvlflllisy
AFIVQAVLRIQSAEGRRKAFGTGSHLLVVSLFYGTAISMYLQppspsskdrckmyll
FCGIIAPMLNPLIYTLRNKEVKEAFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNF
SASCPIFVITIENYCNLPQRKFP"
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/protein_id="CAC20513...
/db_xref="GI:12054411"
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/chromosome="6"
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                                                            Ehlers, n.
Direct Submission
Conhmitted (06 NOV-2000) Ehlers
Conhmitted (harite,
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Younger,R.M., Amadou.C., Bethel,G., Ehlers,A., Fischer Lindahl,K.,
Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J.,
Volz,A., Zlegler,A. and Beck,S.
Characterisation of clustered MHC-linked Olfactory Receptor Genes
in Human and Mouse
                                                                                                                                                                                                                                                                                                                      Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J., Volz, A., Younger, R.M. and Beck, S.
Polymorphisms in olfactory receptor genes: a cautionary no unpublished
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2 Tiegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J., Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S. Polymorphic olfactory receptor genes and HLA loci co
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BM28
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Ehlers, A., Beck, S., Forbes, S.A.,
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ATTGTCCAAGCAGTGTTGAGAATCCAGTCTGCTGAAGGTCAACGAAAGGCATTTGGGACA
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/product="olfactory receptor"
/protein_id="CAC20504 1"
/db_xref="G1:12054393"
/db_xref="G1:12054393"
/translation="MNNAYNKSVPQEFILLVESDQPWLEIPPFVWFLFSYILTIFGNLT
IILVSHVDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICNTRKVISYGGCVAQLF
IFLALGSTECLLLAVMCFDRFVAICRPLHYSIIMHQRLCFQLAAASWISGFSNSVLQS
IWTLKMPLCGHKEVDHFFCEVPALLKLSCVDTTANBAELFFISVFLLIFVFTLILISY
AFIVQAVURIOSAEGGRRAFGTCGSHLIVVSLFYGTAISMYLQPSPSSSKDRGKMYSL
FCGIIAPMLNPLIYTLRNKEVKEAFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNF
SASCPIFVITIEMYCNLPQRKFP"
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2 (bases 1 to 1074)
Ziegler, A., Ehlers, A., Forbes, S.A.,
Younger, R.M. and Beck, S.
Polymorphisms in olfactory receptor
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Characterisation of clustered MHC-linked Olfactory Receptor Genes
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IFLALGSTECLLLAVMCFDRFVAICRPLHYSILMHQRLCFQLAAASMISGESUSVJQS
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2 (bases 1 to 1074)
2 legler,A., Ehlers,A., Forbes,S.A., Trowsda
Younger,R.M. and Beck,S.
Polymorphisms in olfactory receptor genes:
Unpublished
3 (bases 1 to 1074)
                                                                                                                                                                                                                                            Direct Submission
Submitted (06-NOV-2000) Ehlers
Universitaetsklinikum Charite,
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Younger, R.M., Amadou, C., Bethel, G., Ehlers, A., I
Forbes, S.A., Horton, R., Milne, S., Mungall, A.J.,
Volz, A., Ziegler, A. and Beck, S.
Characterisation of clustered MHC-linked Olfacto
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1 (bases 1 to 1074)
2 legler, A., Ehlers, A., Forbes, S.A., Trowsdale, J.,
Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S.
Polymorphic olfactory receptor genes and HLA loci constitute
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MHC-linked olfactory
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Ehlers, A., Beck, S., Forbes, S.A.,
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/protein_id="CAC20506.1"
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/db_xref="GI:12034397"
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Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., F
Forbes,S.A., Horton,R., Milne,S., Mungall,A.J.,
Volz,A., Ziegler,A. and Beck,S.
Characterisation of clustered MHC-linked Olfacto
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Younger,R.M. and Beck,S.
Polymorphisms in olfactory receptor genes:
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Ehlers, A., Beck, S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/chromosome="6"
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MHC-linked olfactory receptor loci exhib
contribute to extended HLA/OR-haplotypes
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2 (bases 1 to 1074)
Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale
Younger, R.M. and Beck, S.
Polymorphisms in olfactory receptor genes: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-NOV-2000)
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Direct Submission
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Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Tro
Volz,A., Ziegler,A. and Beck,S.
Characterisation of clustered MHC-linked Olfactory
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Ehlers, A., Beck, S.,
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Twtlkmplcghkevdhffgevpallklscydttaneaelffisvlflllisy
Afivqavlrigsaegqrafgfgshllvvslfygtaismylqppspsskdrgkwsl
Afivqavlrigsaegqrafgfgshllvvslfygtaismylqppspsskdrgkwsl
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/protein_id="CAC20508.1"
/db_xref="GI:12054401"
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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AJ302589.1 GI:12054402
6M1-10*01 gene; olfactory receptor.
1 (bases 1 Ziegler,A.,
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                                                                                                        CCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTTCCTATATCTTGACAATCTTT
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tttttcttaccaatctatcactcctggatctttgttacaccacatgtacagtcccacaa
                                                                                                                                                                                ATGAATTGGGTAAATAAGAGTGTCCCACAGGAGTTCATTCTGTTAGTTTTCTCAGATCAA
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(in) Kasahara,M. (Ed.);
MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-NOV-2000) Ehlers A., Institut fuer Immungenetik, Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer Lindahl,K. Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J., Volz,A., Ziegler,A. and Beck,S. Characterisation of clustered MHC-linked Olfactory Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehlers, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished 5 (bases 1
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MHC-linked olfactory receptor loci exhibit
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/protein_id="cAc20509; l"
/protein_id="cAc20509; l"
/db_xref="Gi:12054403"
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/translation="mnwvnksvpoefillvfsvpopwlvnicwfkysgogcvaolf
iilvsbyoffklhtpmvfflskusildlcyttsvpopwlvnicwfkkysgogcvaolf
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TWTLKWPLCGHKEVDHFFCEVPALLKLSCVDTTANEAELFFISVLFLLLVTLLILSV
AFIVQAVLRIQSAEGQRKAFGTCGSHLIVVSLFYGTAISMYLQPPSPSSKDRGKMVSL
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SASCPIFVITIENYCNLPQRKFP"
1 248 c 202 g 346 t
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86.38;
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                                                                                                                                                                                                                                                   9 Pred. No. 2.8e. 0; Mismatches
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HLA loci constitute
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                                                                                                                                                      Homo sapiens
AJ302590
AJ302590.1
                                                                    1 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J.,
Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck
Springer-Verlag, Tok 2 (bases 1 to 1074)
                    FUNCTION: 110-130;
                             MAJOR HISTOCOMPATIBILITY
                                                 extended haplotypes
                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                         Homo sapiens
                                                                                                                                            6M1-10*01
                                                           Polymorphic olfactory receptor
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                                        (in) Kasahara,M.
                                                                                                                                    human.
                                                                                                                                                                            sapiens
                                                                                                                                            gene;
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6M1-10*01
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         Tokyo, Japan
                                        (Ed.);
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gene
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r genes and HLA
                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                          olfactory receptor,
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                                                                                                      Hominidae;
                                                             Beck
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cell line
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                                                                                           ccttggctggagtttccactcttgtggtcttcttgatttcttacactgtgaccatcttt 120
cttttcatatttctggccttgggggctactgaatatcttctcctggccgtcatgtccttt
                                                  atgctagtaaatttatgcagcatcaggaaagtaatcagttatcgtggctgtgtgtagcccag
                                ATGCTGGTAAACATATGCAACACCAGGAAAGTAATCAGTTATGGTGGCTGTGTGGCCCAG
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Submitted (06-NOV-2000) Ehlers
Universitaetsklinikum Charite,
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MHC-linked olfactory receptor loci exhibit polymorphism contribute to extended HLA/OR-haplotypes
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Younger,R.M., Amadou,C., Bethel,G.,
Forbes,S.A., Horton,R., Milne,S., M.
Volz,A., Ziegler,A. and Beck,S.
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Ehlers,A., Beck,S., Forbes,S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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SASCPIFVITIENYCNLPORKFP"
3 248 c 202 g 346 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mnwvnksvpqefillvfsdqpwleippfvwflfsyiltifgnlt
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IFLALGSTECLLLAVWCFDRFVAICRPLHYSIIMHQRLCFQLAAASWISGFSNSVLQS
TWTLKMPLCGHKEVDHFFCEVPALLKLSCYTTANABELFFISVGFLLLTSY
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/protein_id="CAC20510.1"
/db_xref="GI:12054405"
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/db_xref="taxon:9606"
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86.3%;
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                                                                                                                                                                                                                                                                                                                                                Score 726.2; DB 9;
Pred. No. 2.8e-197;
0; Mismatches 128;
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younger, R.M., Amadou, C., Bethel
Younger, R.M., Amadou, C., Bethel
Forbes, S.A., Horton, R., Milne, S
Volz, A., Ziegler, A. and Beck, S.
                                                                  Springer-Verlag, Tokyo, Japan (2000)
2 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J.,
Younger,R.M. and Beck,S.
Polymorphisms in olfactory receptor genes: a cauti
                                                                                                                                                                                                   Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J. Uchanska-Ziegler,B., Volz,A., Younger,R. and Bec Polymorphic olfactory receptor genes and HLA loc
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AJ302591.1 GI:12054406
6M1-10*01 gene; olfactory receptor.
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                                                                                                                                                                                        extended haplotypes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens 6M1-10*01 gene
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               Milne,S.,
                              Bethel, G., Ehlers, A., Fischer Lindahl, K.,
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                Mungall, A.J.,
                                                                                                                                                               STRUCTURE,
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loci constitute
                                                                        cautionary note
                  Trowsdale,
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Submitted (06-NOV-2000) Ehlers
Universitaetsklinikum Charite,
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MHC-linked olfactory
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/product="olfactory receptor"
/protein_id="CAC20511.1"
/protein_id="CAC20511.1"
/translation="MNWVNKSVPQEFILLVFSDQPWLEIPPFVMFLFSYILTIFGNLT
/ILVSHYDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICNTRKVISYGGCYAQLF
IILVSHYDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICNTRKVISYGGCYAQLF
IFLAGSTECLLLAVWGDRFYAICREHYSILMHQBLCFGQLAAASMISFSSNSVDRSSNSTRTLKHSYLTHLIFYTLLIISY
AFIVQAVLRIGABGGRKAFGTCGSHLIVVSLFYGTAISMYLDPSPSSKDRRSKNYSL
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248 c 202 g 346 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (bases 1 to 1074)
2iegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J.,
Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck
and Ziegler,A.
MHC-linked olfactory receptor loci exhib
contribute to extended HLA/OR-haplotypes
                                                                                               Younger, R.M., Amadou, C., Bethel, G., Ehlers, A., Fischer Lindahl, K., Forbes, S.A., Horton, R., Milne, S., Mungall, A.J., Trowsdale, J., Volz, A., Ziegler, A. and Beck, S. Characterisation of clustered MHC-linked Olfactory Receptor Genes
                                                                                                                                                                                                  Ziegler, A., Ehlers, A., F
Younger, R.M. and Beck, S.
                                                                                                                                                                                                                                                          MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, FUNCTION: 110-130;
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(in) Kasahara, M. (E
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AJ302592
AJ302592.1 GI:12054408
                                           Ehlers, A., Beck, S.,
                                                                                                                                                                       Unpublished
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2 (bases 1 to 1074)
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                                                              accctgactctccagctgccactctgtgacccctatgtgatagatcactttctctgtgaa
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Direct Submission
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ACCESSION VERSION KEYWORDS RESULT 13 HS193B12/c DEFINITION HS193B12 100375 bp DNA PRI 23-NOV-1999
Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3.
Contains histone Pt2h/d, H2B/d, H2A.1, H1.5, H3.F, H4.k, H3/f
genes, histone Pt2b.1 and hypothetical protein A4 pseudogenes,
histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene,
olfactory receptor OL1 like gene, ESTs STSs and predicted CpG Z98744.1 GI:3080457 6p21.3-22.3; A4; CpG island; Glycine tRNA; H1.5; H2A; H2A.1; H2A.1; H2A/d; H2B; H2B.2; H2B/d; H3; H3.1; H3.F; H3/j; H4; H4.K; h1stone;

Locus

SOURCE ORGANISM

0L1;

olfactory receptor; pH2b.i.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 100375) Homo sapiens Euteleostomi;

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

(http://wwwsanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: colonerequest@sanger.ac.uk on Apr 24, 1998 this sequence version replaced gi:2578067.
IMPORTANT: This sequence is the entire insert of clone 193B12.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with Submitted (12-DEC-1997) Chromosome 6 Project Group Direct Submission

only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed in collaboration by the Sanger Centre chromosome 6 mapping group and Armin Volz & Andreas Ziegler,

according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The true left end of clone 193B12 is at 1 in this sequence. The David Ruddy, Jeffrey Gruen.

Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/ This sequence has been finished

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 true right end of clone 193B12 is at 100375
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/note="match: 5' EST H54606"
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AA061654 H15508 W41535 AA272868 AA453105 W65215 AA231513
AA073767 AA528953 AA492640 W11262 AA060372 AA027719
AA143419 U90551; match: CDNAs L19778 L19779 X58069 X14850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="H2B.1 and H2B.2 like; match: ESTS AA354038 AA217829 W49399 AA396588 AA080125 W41523 AA218213 AA423665 AA562098 AA4992023 AA237861 W41584 AA255145 AA327803 AA064568 AA0956051 W73546 AA493453 AA315768 AA280257 R76857 AA256738 M42065 N99711 N31296 N31249 W71872 AA255154 N28495 AA3266035 N99711 N31296 N31249 W71872 AA255154 N28495
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/gene="H2A/d"
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incomplete repeat"
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/clone="RP1-193B12"
/clone_lib="RPCI-1"
/db_xref="SPTREMBL:Q99877"
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VLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mSGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERV
GAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVT
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/product="histone H2A"
complement(1589. .2087)
/gene="H2A/d"
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x05862 y00117 x16148 z30940 u62674 x57138 u62669 x02218
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/db_xref="taxon:9606"
                                                                           /protein_id="CAB11418.1"
/db_xref="GI:3080459"
                                                                                                                                  /evidence=not_experimental
/product="histone H2B"
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/product="histone H2B"
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'product="histone H2A"
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db_xref="GI:3080458"
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P27795 CE05165
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             /note-"match: proteins Q90859 P06899 P10854 P23527 P33778 Q64524 P06900 P02279 P02278 P02281 P10853 Q64477; match: ESTS AA256738 AA327803 AA286933 AA315768 AA286932 AA280257 AA493453 AA423665; match: cDNAs M18046 M18045 M69756 M25487; match: genomic DNAs X83547 Z83336 Z80780 U62669
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/note="match: 5'
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7038. .7077
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                                                                                   complement(27803. .28142)
/gene="pH2B.i"
                                                                                                                                 complement(27803.
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17170. .17463
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noomplete repeat"
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[1933. .11977
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1786. .5085
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                                                           caaccaccttcgcccagctccaaggaccaaggaaagatggtttctctcttctatggaatc
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28508. .28807
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27829. .29369
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86.3%;
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Pred. No. 3.8e-197;
0; Mismatches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7272173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., I
Anderson, S., Baldwin, J., Barna, N.,
                                                                                                                                                                                                                                                                                               1 (bases 1 to 166758)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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SEQUENCE, 17 unordered pieces
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                             Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 156318 bases at least Q30 Consensus quality: 161224 bases at least Q30 Consensus quality: 161245 bases at least Q30 Consensus quality: 163451 bases at least Q30
Insert size: 191000; agarose-fp
Insert size: 165158; sum-of-contigs
Quality coverage: 4.0 in Q20 bases;
Quality coverage: 4.6 in Q20 bases;
                                                                                                                                                                               Center project name: L6934 Center clone name: 598_O_1
                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                               Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                             Genome
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17 37679: contig of 9033 bp in le

30 37779: gap of 100 bp

30 45607: contig of 7828 bp in le

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4447. .7420
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note="assembly_fragment"
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46: gap of 100 bp
37679: contig of 9033 bp in
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CCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTTCCTATATCTTGACAATCTTT

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ggcaatctgaccattattctagtgtcacgcctggacaccaaaacttcatacccccatgtat 180

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accctgactctccagctgccactctgtgacccctatgtgatagatcactttctctgtgaa

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ACCTGGACACTTAAGATGCCACTGTGTGGTCACAAAGAAGTGGATCACTTCTTCTGTGAA

tgcctccagttggcagcagcatcctgggttactggttttagtaactcagtgtggttgtct 480 GATAGGTTTGTAGCTATTTGTCGGCCTCTCCATTACTCAATTATCATGCACCAGAGGCTC gataggtttgtagctatttgtcggcctctccattactcagttatcatgcaccagagactc CTTTTCATTTTCCTGGCCTTGGGTTCCACAGAATGTCTTCTCCTGGCCGTCATGTGCTTT

TGCTTCCAGTTGGCAGCTGCATCCTGGATTAGTGGCTTTAGCAATTCAGTATTACAGTCC

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TGTGGCTCCCATCTAATTGTGGTGTCACTTTTTTATGGTACAGCTATCTCCATGTACCTG

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                                                                                              /note="assembly_fragment"
77943. 98659
                                                                                                                          63831
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54540. .63730
              /note="assembly_fragment"
33823 c 33960 g 48591
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45708. .54439
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 ATGAATTGGGTAAATAAGAGTGTCCCACAGGAGTTCATTCTGTTAGTTTTCTCAGATCAA 99399
                                                                 77.1%;
86.3%;
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                                                       Mismatches 128;
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AC025941
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Nell,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Stange-Thomann,N., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Schauer,S., Severy,P., Spencer,B.,
Trigillo,J.,
Tirrell,A., Travers,M., Trigillo,J.,
Vene and Markey B. M., Stanger, M., Trigillo,J.,
Vene and Markey B. M., Stanger, M., Trigillo,J.,
Vene and Markey B. M., Stanger, M., Trigillo,J.,
Vene and M., Stanger, M., Trigillo,J.,
Vene and Markey B. M., Stanger,M., Trigillo,J.,
Vene and M., Stanger, M., Trigillo,J.,
Vene and M., Stanger,M., Trigillo,J.,
Vene and M., Stanger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:7259782.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dedar, R., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dedar, R., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dedar, R., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dedar, R., De
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SEQUENCE, 15 unordered piece
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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HTG; HTGS_PHASE1; HTGS
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 16829 bases at least Q40
Consensus quality: 172827 bases at least Q30
                                                                                                                                                                                                 Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                               Center project name: L8577 Center clone name: 635_0_1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                              Project Information
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ne 6, clone
                                                                                                                                                                                                                                                                                          635_0_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currentle consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 176000; agarose-fp Insert size: 174877; sum-of-contigs Quality coverage: 4.5 in Q20 bases; Quality coverage: 4.6 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality:
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131999 176277: contig of 44279
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70420: contig of 11305 bp in length
70520: gap of 100 bp
80466: contig of 9946 bp in length
80566: gap of 100 bp
92325: contig of 11759 bp in length
92455: gap of 100 bp
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ALIGNMENTS

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RESULT
AAS08541
CDS
                 Walke DW, Wilganowski NL, Zambrowicz B, Sands AT;
                                                                 12-JAN-2000; 2000US-0175764
                                                                                    05-JAN-2001; 2001WO-US00589
                                                                                                      19-JUL-2001.
                                                                                                                           WO200151634-A1.
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                diagnostic; ss.
                                                                                                                                                                                                                         Human; novel G-protein coupled receptor; NGPCR; drug discovery;
                                                                                                                                                                                                                                           DNA encoding novel human G-protein coupled receptor (NGPCR).
                                                                                                                                                                                                                                                               26-SEP-2001
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                                              (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                               Location/Qualifiers
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/product= "Novel G-protein coupled receptor (NGPCR)"
                           Turner CA,
                           Friedrich G,
                           Abuin
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WPI; 2001-442145/47

P-PSDB;

AAU04689

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Claim
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Page 61;
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New human G protein-coupled receptor and polynucleotides encoding the receptor, useful in identifying, selecting or validating new molecular targets for drug discovery and in diagnostic or prognostic assays 65pp; English.

The sequence represents the coding sequence of novel human G-protein coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful in identifying, selecting or validating novel molecular targets for drug discovery, as well as in diagnostic or prognostic assays. These are also useful in microarrays or other assay formats, for screening collections of genetic material from patients who have a particular medical condition or for identifying mutations associated with a particular disease. condition

Sequence 942 ₿₽; 222 A; 228 C; 187 ç; 305 T; 0 other;

Query Match Best Local

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05-JAN-2001; 2001WO-US00589

12-JAN-2000; 2000US-0175764.

(LEXI-) LEXICON GENETICS

Zambrowicz Walke W Wilganowski NL, B, Sands AT; Turner CA, Friedrich ç, Abuin

WPI; 20 P-PSDB; 2001-442145/47. DB; AAU04689.

New human G protein-coupled receptor and polynucleotides encoding receptor, useful in identifying, selecting or validating new molectargets for drug discovery and in diagnostic or prognostic assays molecular

Disclosure; Page 62-63; 65pp; English.

The sequence represents the open reading frame (ORF) encoding novel human G-protein coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful in identifying, selecting or validating novel molecular targets for drug discovery, as well as in diagnostic or prognostic assays. These are also useful in microarrays or other assay formats, for screening collections of genetic material from patients who have a particular medical condition or for identifying mutations associated with particular disease.

Sequence 1488 BP; 421 Α; 333 ç; 254 G; 477 T; 3 other;

Query Match Best Local S Matches 942 Local Similarity Conservative 100.0%; 0, Score 942; DB 22; Pred. No. 1.7e-279; Mismatches 0; Length Indels 0; Gaps 0

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Human
olfactory receptor
polynucleotide,
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secondary ; olfactory receptor; OR; primary scent determinat. dary scent determination; polypeptide library; odoprofile; scent fingerprint; scent representation; determination; odour i receptor;

Homo sapiens

WO200127158-A2

19-APR-2001

06-OCT-2000; 2000WO-US27582

08-OCT-1999; 24-FEB-2000; 99US-0158615 2000US-0184809

DIGISCENTS YEDA RES &

RES & DEV င္ပ

2001-290713/30 Ţ, Smith Ď Lancet Ď Glusman ç, Fuchs 'n, Yanai Į,

Claim

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Page 417;

English.

 $\begin{array}{l} \mathbb{Z}\times \mathbb{Z}$

New polynucleotides sensation for identi otides which identifying 1857pp; encode polypeptides olfactory agonists a s involved in olfactory and antagonists -

which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary sensts and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detection of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of olfaferences in the olfactory faculties. faculties

Sequence 939 В₽; 220 Α; 227 ç; 187 G; 305 Τ; 0 other;

Match

Length

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Best Loc
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RESULT
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standard;

DNA; 939 ВP

30-JUL-2001 AAH32018; AAH32018

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RESULT
AAH31.669
ID AAH3
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Claim Page 273-274; 1857pp; English.

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Query Match Best Local Similarity

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RESULT AAC77475 AAC77475 standard; 08-FEB-2001 ORF3030 polynucleotide sequence SEQ ID (first entry) CDNA; 1442 ВP

NO:6059.

anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID, AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulati vulnerary; antipsoriatic; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; Human; open reading frame; ORFX; detection; thrombosis; contraceptive; cytostatic; hepatotropic; nootropic; neuroprotective;

05-OCT-2000

31-MAR-2000; 2000WO-US08621

31-MAR-1999; 02-APR-1999; 05-APR-1999; 30-MAR-2000; 99US-0127607. 99US-0127636. 99US-0127728. 2000US-0540763.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach

2000-602362/57

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy
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immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
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Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour r scent profile; scent fingerprint; scent representation; ds. AAH32304 standard; Human olfactory receptor polynucleotide, 30-JUL-2001 æ sapiens profile; (first entry) DNA; 939 ВÞ SEQ IJ ö odour receptor;

W0200127158-A2

19-APR-2001

06-OCT-2000; 2000WO-US27582

08-OCT-1999; 24-FEB-2000; 2000US-0184809 99US-0158615

(DIGI-) DIGISCENTS.
(YEDA) YEDA RES & DEV CO LTD

Bellenson Ū, Smith D, Lancet Þ Glusman Ġ Fuchs H, Yanai

2001-290713/30

New polynucleotides sensation for identi tides which identifying encode polypeptides olfactory agonists a s involved in ol and antagonists olfactory sts -

Claim 8 Page 530; 1857pp; English.

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to these primary scents. The methods also enable the identification of determination o detect

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                                                 atcacatccatgttgaactccctcatctacagccttagaaataaagatatgaaggaggcc
 939
                                                  900
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RESULT AAH31645 standard; 9 DNA; ВР

Human olfactory receptor polynucleotide, 30-JUL-2001 (first entry) SEQ ij NO:

Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour r scent profile; scent fingerprint; scent representation; ds. determination;
ibrary; odour receptor;

sapiens.

WO200127158-A2

06-OCT-2000; 2000WO-US27582

08-OCT-1999; 99US-0158615 24-FEB-2000; 2000US-0184809

(YEDA) YEDA RES & & DEV CO LTD

Bellenson Smith Lancet 'n Glusman ć Fuchs Ţ,

New polynucleotides which encode polypeptides involved in ol sensation for identifying olfactory agonists and antagonists

Claim 8; Page 263; 1857pp; English

AÄH31645
ID AAH3
XX AAH3
AC AAH3
XX 30-J
DX 30-J
DX W Secco
KW Sec The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties of different individuals.

Sequence 936 BP; 222 A; 226 C; 188 ç; 300 T; 0 other;

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Db
dq
                                        В
                                                          δÃ
                                                                                          Query Match
Best Local Similarity
                                                                                  Matches 593;
                                                   atgaattgggtaaatgacagcatcatacaggagtttattctgctgggtttctcagatcga
                                       atggatcagaaaaatggaagttctttcactggatttatcctactgggtttctctgacagg
                                                                                  Conservative
                                                                                           42.5%;
                                                                                Score 400.4; I
Pred. No. 5.2e
0; Mismatches
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5.2e-113;
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ccttggctggagtttccactccttgtggtcttcttgatttcttacactgtgaccatcttt 120

cctcagctggagctagtcctctttgtggttcttttgatcttctatatcttcactttgctg

120

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AC AAH5
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                   Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
                                                                       Human olfactory receptor polynucleotide,
                                                                                                 30-JUL-2001
                                                                                                                                                 AAH32063 standard;
Homo sapiens
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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                            Claim 8; Page 435-436;
                                                                                                                                                                                                                                                                                                                                                                  Bellenson J,
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24-FEB-2000;
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                            of different individuals.
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and antagonists
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Sequence 1002 BP; 210 Α, 266 ç; 217 G; 309 T; 0 other;

faculties

Query Match Best Local Sim Matches 580;

Similarity

39.3%;

Conservative

0; Score Pred.

Mismatches

0,

Gaps

0

370; No. 1.

DB 22; l.2e-103;

Length Indels

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δ. β.
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RESULT 1
AAH32306
ID AAH3
XX AAH3
XX AC
DT 30-J
XX Huma
XX Huma
XX Homc
KW Scert
XX Homc
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                            Claim
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                                                                                                                                                                                                                                                                                                                                    08-OCT-1999; 99US-0158615.
24-FEB-2000; 2000US-0184809.
                                                                    New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
                                                                                                                                                                                                      Bellenson J,
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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors and can be used for determining differences in the olfactory faculties different individuals.

Sequence 1011 BP; 217 A; 252 C; 202 G; 340 T; 0 other;

Query Match Best Local Similarity

38.7%;

Score 364.2; DB 22 Pred. No. 7.3e-102;

22;

Length 1011

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g QYď ΩY g ΛĊ gg. νQ В Qy Ü · Ω γQ Q . Qy Ъ δÃ В Db DЬ g Q. g ÇΥ Ŗ 20 Matches 189 489 492 429 369 309 249 192 69 agctatttgtcggcctctccattactcagttatcatgcaccagagactctgcctccagtt tctaattgtggtgtctcttttttatagtacagccgtctctgtgtacctgcaaccaccttc agtattgaggatacagtctgctgaaggtcgacaaaaagcatttgggacatgtggttccca ccagctgccactctgtgacccctatgtgatagatcactttctctgtgaagtccctgcact tctggccttgggggctactgaatatcttctcctggccgtcatgtccttttgataggtttgt tttatgcagcatcaggaaagtaatcagttatcgtggctgtgtagcccagcttttcatatt aaateteteatttetggatetetgetacaeeaceagetetateeeteagttgetggtgaa caatctatcactcctggatctttgttacaccacatgtacagtcccacaaatgctagtaaa gtttccactccttgtggtcttcttgatttcttacactgtgaccatctttggcaatctgac tettatggttgtatetetetttteatteeagteatgtgcatgtateteeageeaceate tgtactgagcatgcaatcaaccactgggcttcagaaagtgcttaggacatgtggagccca tctgcgattatcatgtgttgatacctaggcaaatgagctgaccctcatggtcatgagctc gctcaagttatcttgtgttgagacaacagcaaatgaggctgaactattccttgtcagtga ctggatacccctatgtagacatcgcctagtggatcacttcttctgtgaagctccagcact ggctgcggcttcttgggtaagtggttttacaacctcagcacttcattcctcctttacttt ggcagccgcatcctgggttactggttttagtaactcagtgtggttgtctaccctgactct tctcgcactgggaaccgcagagtgtgtcctactggtggtgatgtcctatgatcgttatgc tctctggggcccggaaaagaccatctcttatgctggttgtacagttcaactttactttgt catcatcatcctgtcatacctggactcccatctccacactcccatgtacttcttcctttc agtagttctctttgtggttatcttgatcttctacttgataacactgataggaaacctgtt agctgtgtgtagacctttgcattacactgtcctcatgcaccctcgtttctgccgcttgtt Conservative 0; Mismatches 333; Indels 0 491 728 611 551 488 188 191 131 89 791 731 899 671 809 548 368 371 308 311 248 251

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24-FEB-2000;
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Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour r scent profile; scent fingerprint; scent representation; ds.

receptor;

Homo sapiens

Human olfactory receptor polynucleotide,

SEQ ID NO:

30-JUL-2001

(first entry)

AAH32314 standard;

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                                                        New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
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present sequence is one of a number

of isolated polynucleotides

Page 437; 1857pp;

English.

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New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -

Claim 8; Page 428-429; 1857pp; English.

scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent ingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties of different individuals The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary of different individuals.

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Sequence 936 BP; 180 A; 273 C; 243 G; 240 T; 0 other;

Matches Query Match Best Local Similarity Conservative 37.4%; 0 Pred. Mismatches 352.4; DB No. 3e-98; 356; Indels Length 0, Gaps

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A04 1 atgaattgggtaaatgacagcatcatacaggagtttattctgctgggtttctcagatcga atggacggggtgaatgatagctccttgcagggctttgttctgatgagcatatcggaccat 60 60

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                                                                                                                                         ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-827-291A-1
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Query Match
Best Local Similarity
Matches 482; Conserv
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                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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444443387543310
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LENGTH: 1290 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: 28-MAR-1CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Sathe, Ganesh
TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR
NUMBER OF SEQUENCES: 2
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US-08-842-235B-3
US-08-629-335B-3
US-07-866-560-3
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                        Score 216.8;
Pred. No. 4.
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   Mismatches
                           .8; DB 2;
4.7e-60;
                                                   Length 1290;
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Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score

Match Query

Length

DB

Description

200 197.2

216.8 211.6 211 200.8 200.8

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US-08-827-291A-1
US-08-748-506-7
US-08-748-506-8
US-08-467-947A-1
US-08-467-947A-1
US-08-465-947-1
US-08-748-506-6
US-08-748-506-6
US-08-748-506-9
US-08-748-506-9
US-08-98-876-2
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US-08-997-252-83
US-08-671-5558-3

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*

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/cgn2_6/ptodata/2/ina/backfiles1.seq:*

Minimum DB Maximum DB

seq

length:

length: 2000000000

Total number of hits satisfying chosen parameters:

702406

351203 seqs, 113238999 residues

Searched:

Scoring table: Sequence:

IDENTITY_NUC Gapop 10.0 ,

Gapext 1.0

Perfect score:

US-09-755-017-1 942

atgaattgggtaaatgacag...

.....tcttcttaatcaagaaataa

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RESULT 2
US-08-748-506-7
Sequence 7, Application US/08748506
Patent NO. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM
NUMBER OF SEQUENCES: 31
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SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILLING DATE: 08-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION
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ADDRESSEE: Leydig, Voit & Mayer, Ltd
STREET: Two Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Pr
CITY: Chicago
STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                      ctggccgtcatgtcctttgataggtttgtagctatttgtcggcctctccattactcagtt 402
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aatgaggctgaactattccttgtcagtgagctcttccatctaatacccctgacactcatc
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Pred. No. 1.9e-58;
0; Mismatches 334;
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                                                                                                                                                                                                                                             TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                           Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL
                                                                                                                                                                                                                         TOPOLOGY: 1in MOLECULE TYPE:
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                                                          661
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                                                                                                                           Local Similarity
les 415; Conserv
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FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                  acatgtacagtcccacaaatgctagtaaatttatgcagcatcaggaaagtaatcagttat 282
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GCCCTCTTCTATACATCAGTGACATCCATGCTGAATCCCATCATCTACAGCTTAAGGAAC 900
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Pred. No. 3e~58;
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AAGGATGTCAAGGCAGCACTGAGAAGAATTCTGGC
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US-08-467-948A-1
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GENERAL INFORMATION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                     TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR2 NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                            APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                          STREET:
CITY: W
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
                                                                                                 COUNTRY: US
ZIP: 20005
                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                        WASHINGTON
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US-08-467-948A-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/04079 FILING DATE: 30-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 1713 base pairs
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JS-08-467-947A-1
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                                                                                                                                                       TELEFAX: 202-37
INFORMATION FOR SEQ
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/
APPLICATION NUMBER: 957-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
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                                             FEATURE:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          TELEPHONE: 202-371-2600
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                                                              MOLECULE TYPE:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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                                                                                          STRANDEDNESS:
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             LOCATION:
                              NAME/KEY:
                                                                             TOPOLOGY:
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1100 NEW YORK AVE., NW, SUITE 600
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
             CDS
116..1003
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RESULT 6
US-09-085-371-5
US-09-085-371-5
Sequence 5, Application US/09085371
Sequence 10, 6218358
Patent No. 6218358
GENERAL INFORMATION:
APPLICANT: Firestein, Stuart
APPLICANT: Zhao, Haiqing
TITLE OF INVENTION: Functional Ex
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Pred. No. 7.9e-55;
  Expression
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SEQ ID NO 5
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Best Local
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CURRENT FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: US 08/891,243
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: US 60/045,961
PRIOR FILING DATE: 1997-05-07
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SOFTWARE: PatentIn version
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Pred. No. 1e-54;
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REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-007-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ATTORNEY/AGENT INFORMATION
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                                                                                  APPLICATION NUMBER: US/OFFILING DATE: 08-NOV-1996 CLASSIFICATION: 435
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TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity
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AAGGAAGTCAAGGCAGCACTGAGAAG
              aaggaggtaaaggaaggctttaaaag 908
                                                                                                                                                                            CATAAAGCTCTTTCCACCTGTTCCTCACACCTACTTGTAGTCACACTCTTTTATGGCTCT
                                                                                                                                                                                              caaaaagcatttgggacatgtggttccccatctaattgtggttgtctcttttttatagtaca
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                                                                                                                 GTGTCCTTTACCTATTTGAGGCCCAAGTCTAGCCACTCACCAGGAATGGACAAACTCTTG
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Pred. No. 1.3e-51;
0; Mismatches 348;
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RESULT 9 US-08-748-506-9

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Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
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LENGTH: 984 base pairs
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APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
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APPLICATION NUMBER: US
FILING DATE: 08-NOV-19
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version
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                                                                            ctggccttgggggctactgaatatcttctcctggccgtcatgtcctttgataggtttgta
                                                                                                                     ATTCTGTCAGGGAGGCAAAAGATTCCCTTTGGGGTCTGCTTCTCACAGGCCTTCGTCTAT
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ttatgcagcatcaggaaagtaatcagttatcgtgggctgtgtagcccagcttttcatattt
                                                          CTTGTCGTGGGGGCAACAGGTTTTTTCCTTTTGGCTGCGTTATCCCTGGACCGCTTTCTG
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312-616-5700
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RESULT 10
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                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Soppet
                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1474 base pairs
                                                                                                  NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
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CITY: R
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Li, Yi
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Matches 317
                                                                                                                                                                                                       Sequence 1, Application Patent No. 5948890
                                                                                                                                                                                         GENERAL INFORMATION:
                                                              APPLICANT: ROSEN, Craig A.
APPLICANT: Ruben, Steeven M.
TITLE OF INVENTION: HUMAN G-PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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Roseland
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                6 Becker Farm Road
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Li, Yi
                              CARELLA, BYRNE, I
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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mes 317; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sing
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REGISTRATION NUMBER: 36,
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Best Local Similarity
Matches 317; Conserv
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GENERAL INFORMATION:
APPLICANT: Soppet
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
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STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/465,980
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                                                                                                                             Score 118.4; DB 5;
Pred. No. 2.6e-28;
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                                                                                                                                   Indels
                                                                                                                                                                  Length
                                                                                                                                                                  1474;
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                                                                                                                                 Gaps
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US-08-988-876-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: I
APPLICANT: I
APPLICANT: I
                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: G PROTEIN CO
TITLE OF INVENTION: WITH IMMUNE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919
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                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 94304
                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTTTGGAACCTGTGTCACACATTGGTGTGGTACTCGCCTTCTAT 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08988876
                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman, Olga
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yue, Henry
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                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
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                    PF-0441 US
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ŲS-08-988-876-2
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Best Local :
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SEQUENCE CHARACTERISTICS:
1174 ATATCATTCA 1183
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TYPE: nucleic acid
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CLONE: 364702
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                                  ccattactca 399
                                                                                       ---atatetteteetggeegteatgteetttgataggtttgtagetatttgteggeetet 389
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                                                                  GAGAGACATGCTCCTGAGTGTGATGGCCTATGACTGGTTTGTAGCCATCTGTCACCCGCT
                                                                                                                                                                           atcagttatcgtggctgtgtagcccagcttttcatatttctggccttgggggctactga- 332
                                                                                                                                                                                                                  GGTTTCACCTCCACCACGGTCCCCAAGATGATTGTGGACATCCAGTCTCACAGCAGAGTC
                                                                                                                                                                                                                                     tgttacaccacatgtacagtcccacaaatgctagtaaatttatgcagcatcaggaaagta
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                                                                                                                                                                                                                                                                                                            CTGTCCATGTGCCTGGTCACGGTGCTGGGGAACCTGCTCATCATCCTGGCCATCAGCCCT 933
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Pred.
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. No. 1.5e~20;
ismatches 161;
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US-08-599-252-84/c
                                                                                                                                                                                                                                                                                      Sequence 84,
Patent No. 5
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                           APPLICANT:
APPLICANT:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                     APPLICANT:
                                                                               STREET: 2000 Pen
CITY: Washington
STATE: DC
COMPUTER: IBM PC OPERATING SYSTEM:
                                                       ZIP:
                                                                  COUNTRY:
                                                                                                                        ADDRESSEE:
                                                      20006-1888
                                                                                                                                                                                                                                                                                        4, Application US/08599252 5705343
                                                                                                            2000 Pennsylvania Ave. N.W.,
                                                                                                                                                             THOMAS, WINSTON J.
WOLFF, ROGER K.
NVENTION: METHOD TO DIAGNOSE
NVENTION: HEMOCHROMATOSIS
                                                                                                                                                                                                                                  GNIRKE, ANDREAS
                                                                                                                                                                                                                                               DRAYNA, DENNIS T. FEDER, JOHN N.
                                                                                                                                                                                                                    KIMMEL,
                                                                    USA
                                                                                                                       MORRISON & FOERSTER
PC-DOS/MS-DOS
                                                                                                                                                                                                                        BRUCE E
                                                                                                                                                    124
                                                                                                            Suite 5500
                                                                                                                                                                               HEREDITARY
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SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-599-252-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-436-074-57/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%;
Best Local Similarity 65.8%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08436074
Patent No. 5753438
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,074
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1199
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REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELECHOONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1139 GCCATGAAGAAGGTGCTAG 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1319 ACTTGCAGCTCGCATCTAATTGTTGTCTCTCTCTTCTATGGTACAATCATATACATGTAC: 1260
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                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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CLASSIFICATION:
                                                                                                                                                                                            CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)
TELEX: 90-4030
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                                                                                                                                                      ZIP: 20006-1888
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggctttaaaaggttggttg 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCAGCCAGCAAATACTTATTCCCAGGACCAGGGCAAGTTTCTTACCCTTTTCTACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000 Pennsylvania Ave. N.W., Suite $500
                                                                                                                                                                                                                                                                                    GNIRKE, ANDREAS
KIMMEL, BRUCE E.
THOMAS, WINGTON J.
WOLFF, ROGER K.
WOLFF, ROGER K.
VENTION: METHOD TO DIAGNOSE HEREDITARY
VENTION: HEMOCHROMATOSIS
SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                   FEDER, JOHN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202)
                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                  MORRISON & FOERSTER
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Pred. No. 2.9e-19;
                                                          #1.30
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                                                                                                                                                                                                                                            Query Match 9.6
Best Local Similarity 65.8
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1139 GCCATGAAGAAGGTGCTAG 1121
                                                              1199
                                                                                                                       1259
                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                              868
                                                                                                                                    778 ctgcaaccaccttcgcccagctccaaggaccaaggaaagatggtttctctcttcttatgga 837
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 887-0763
TELEFAX: (202) 887-0763
TELEX: 90-4030
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                      TCCAGCCAGCAATACTTATTCCCAGGACCAGGGCAAGTTTCTTACCCTTTTCTACACA 1200
                                                                           atcattgcacccatgctgaatccccttatatatacacttaggaacaaggaggtaaaggaa 897
               ggctttaaaaggttggttg 916
                                                            ATTGTCACTCCCAGTGTTAACCCCCCTGATCTATACACTAAGAAACAAAGATGTTAAAGAG 1140
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                                                                                                                                                                                                                                                            Score 90.2; DB 1;
Pred. No. 2.9e-19;
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Search completed: February 26, 2002, Job time: 4895 sec 05:02:56

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gb_htg:AL592522
gb_htg:AC084042
gb_htg:AC083834
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gb_pr:HSA302542
gb_pr:HSA302543
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gb_pr:HSA302540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_ro:RATOL1RECE
gb_pr:HSA302537
gb_pr:HSA302538
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gb_htg:AC024428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database sequences: 1472140
Database length: -341344837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block: Query: US-09-755-017-2 Query length: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM of: US-09-755-017-2 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time (sec): 1363.720000
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                                                                                                                                                                   gb_htg:AL359352
gb_htg:AL365336
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-Q=/cgn2_1/USPTO_spool/US09755017/runat_25022002_165640_20772/app_query.fasta_1.374
-Q=/cgn2_1/USPTO_spool/US09755017/runat_25022002_165640_20772/app_query.fasta_1.374
-DB=GenEmbl -QRMTP_fastap -SUFFIX=p2n.rge -GAPDD=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL-0.000 -LOOPEXT=0.000
-GAPEXT=0.100 -VGAPEXT=0.500
-FGAPDD=6.000 -GAPEXT=7.000 -YGAPDD=10.000 -YGAPEXT=0.500
-DELOD=6.000 -DELEXT=7.000 -YGAPDD=10.000 -YGAPEXT=0.500
-DELOD=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORD=PCt
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE_LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=20000000
-USER=US09755017_@CGN1_1_5603 -NCPU=6 -ICPU=3 -LONGLOG
-USER=US09755017_@CGN1_1_5603 -NCPU=6 -ICPU=3 -LONGLOG
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14 | L34074 Rat OL1 receptor gene,
2 | AJ302537 Homo sapiens 6M1-1*01
2 | AJ302538 Homo sapiens 6M1-1*01
2 | AJ302540 Homo sapiens 6M1-1*01
2 | AJ302541 Homo sapiens 6M1-1*01
2 | AJ302542 Homo sapiens 6M1-1*01
2 | AJ302543 Homo sapiens 6M1-1*01
2 | AJ302544 Homo sapiens 6M1-1*01
2 | AJ302545 Homo sapiens 6M1-1*01
3 | AJ302545 Homo sapiens 6M1-1*01
4 | AJ302545 Homo sapiens 6M1-1*01
5 | AJ302546 Homo sapiens 6M1-1*02
6 | AJ302546 Homo sapiens 6M1-1*02
7 | AJ302546 Homo sapiens 6M1-1*02
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U86271 Homo sapiens olfactory r
20 AL359352 Mus musculus chromo
21 AL359358 Mus musculus chromo
22 I AL365336 Mus musculus chromo
23 U86275 Homo sapiens olfactory r
25 AL592522 Mus musculus chromo
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AJ302588 Homo sapiens 6
AJ302589 Homo sapiens 6
AJ302590 Homo sapiens 6
AJ302591 Homo sapiens 6
AJ302591 Homo sapiens 6
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! AL589651 Mus musculus chrome
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! AC025941 Homo sapiens chrom
! AL589742 Mus musculus chrom
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   AC083834
AL121944
                                                                    AC084042 Mus musculus chrom
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   Mus musculus chrom
Human DNA sequence
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qb_htg:AC074365
em_htg_hum:AL390860
gb_htg:AC091612
gb_htg:AL357039
gb_pr:HSA302547
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SOURCE
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TITLE
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g., Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1sA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 18, 2000 this sequence version replaced gi:9588470.
During sequence assembly data is compared from overlapping clon where differences are found these are anotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone RP3-408B20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-31316 is at 44689 in this sequence true right end of clone RP1-193B12 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr6
RP3-408B20 is from the library RPCI-3 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For furthen
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: SMBL; Sw: SWHISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Further information can be found
                                      /note="AluSx repeat: matches 3.
932. .1870
                                                                                                                   complement(1. .100)
/note="match: STS:
222. .535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                           /clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                          /clone="RP3-408B20"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/gene="dJ408B20.1"
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1294.60
1294.49
1293.99
1337.26
                                                                                                                                                                                                        .100)
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7.8e-64
7.9e-64
8.4e-64
3.3e-66
                                                                                                                                                                  Em: HS193B12T"
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178295
180657
190889
936 !
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                                                                                 .301 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at 100 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! AC091612 Homo sapie
! AL357039 Homo sapie
AJ302547 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC074365 Homo sapiens ch
Al390860 Human DNA seque
AC091612 Homo sapiens ch
AL357039 Homo sapiens ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further
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```

consensus"

of

consensus"

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(olfactory family) (hS6M1-3P) pseudogene)
match: clnAs: Em:M64392 Em:AF102516 Em:Y15525
Em:X89699 Em:AF102521 Em:AF042016 Em:AF044033 Em:AF102525
Em:AF044034 Em:AF042035 Em:AJ003145 Em:Y1444 Em:AF044037
Em:X10529 Em:AF0102529 Em:AF044038 Em:AF091565 Em:Y07557
Em:X19706 Em:AF042020 Em:M64391 Em:AF02532 Em:AF102533
Em:M64376 Em:AF102535 Em:M64377 Em:M64378 Em:AF102533
Em:M64376 Em:AF102535 Em:M64377 Em:M64378 Em:AF102537
Em:AF102540 Em:M64385 Em:AF091577 Em:M64386 Em:M64387
Em:M64388 Em:AF091580 Em:D12820
Em:M64388 Em:M64388 Em:AF091577 Em:M64386 Em:M64387
Em:M64388 Em:M64388 Em:AF091577 Em:M64386 Em:M64387
Em:M64388 Em:M64388 Em:AF091577 Em:M64386 Em:M64387
Em:AF091573 Em:M64388 Em:AF091578
Em:M64388 Em:AF091578
Em:AF091573 Em:M64388 Em:AF091578
Em:AF091573 Em:M643887
Em:AF091573 Em:M64388 Em:AF091578
Em:AF091573 Em:M643887
Em:AF091573 Em:M64388
Em:AF091573 Em:M64388
Em:AF091573
Em:AF091573 Em:M64388
Em:AF091573
E
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/note="MER76 repeat: matches 613.6753..6850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="4°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="I"
                         /note="AluJb repeat: matches 29. 17090. 17158
                                                                                                                                                                             /note="MIR repeat: matches 58. .199
complement(15225. .15506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6275. .6509
/note="L1M4 repeat: matches 5093.
complement(6590. .6889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="42 copies 2 mer ag 79% conserved" 2559. .2650 /note="2 copies 46 mer 91% conserved" complement(4227. .4576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
complement(1518. .1963)
/note="match: GSS: Em:AQ456128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L2 repeat: matches 2375.
complement(4834. .5686)
                                                                                                                                                                                                                                                                           /note="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7006. .7615
/note="L1P repeat: matches
7611. .9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2024. .2298
/note="AluJo repeat: matches 1. .280 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="dJ408B20.1"
/note="dJ408B20.1
  /note="AluJ/FLAM repeat: matches 1. .81 of consensus"
                                                                            /note="match:
L6824. .17089
                                                                                                                            /note="match: GSS:
15627. .16228
                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ100659"
                                                                                                                                                                                                                                                                                                                                                  'note="MLT1H repeat: matches 1. .168 of
                                                                                                                                                                                                                                                                                                                                                                                                'note="LTR16A repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="HERVL repeat: matches 3244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="LlP repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1P repeat: matches 580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  753. .6850
note="L1P repeat: matches 1. .98 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"match: GSS: Em:U94441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: GSS: Em:AQ748194"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ote="MIR repeat: matches 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "L2 repeat: matches 1381.
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                                                                                                                                                                                                                             13803
                                                                                                   GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 3813.
                                                                                                   Em: AQ544878"
                                                                                                                                                   Em: AQ100750"
                                                                                                                                                                                                                                                                                                  matches 3898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900. .1509 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  203. .307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .776 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .240 of
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                                                .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5344 of
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                                                                                                                                                                                                                                                                                                    .4367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5329 of consensus"
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                                                                                                                                                                                                                                                                                                    consensus"
                                             alignment_block:
US-09-755-017-2 x
Align seg 1/1 to:
                                                                                                                       Percent Similarity:
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                                                                                                                                                                       Quality:
                                                                                                                                                   Ratio:
                                                AL133267
AL133267
                                                                                                                     1601.00
5.115
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Em:M64391
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17789. .18240
/note="match: STS: Em:G31213"
20021. .20249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(21244. .
/note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="dJ408B20.2"
20708. .21649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNWVNDSIIQEFILLGFSDRPWLEFPLLVVFLISYTVTIFGNLT
IILVSRLDTMKHTPMYFFLTMLSLLDLCYTTCTVPQMLVNLCSIRKVISYRGCVAQLF
IFLALGATEYLLLAVMSFDRFVAICRPLHYSVIMHQRLCLQLAAASWVTGFSNSVMLS
TLTLQLPLCDPYVIOHFLCEVPALKLSCVETTANEAELFLVSELFHLIPLTLILISY
AFIVRAVLRIQSAEGRQKAFGTCGSHLIVVSLFYSTAVSVYLQPPSPSSKDQGKMVSL
                                                                                                                                                                                                                                                 /note="AluJb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYGIIAPMLNPLIYTLRNKEVKEGFKRLVARVFLIKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="dJ408B20.2 (novel 7 transmembrane
(olfactory family) (hs6M1-32))"
/protein_id="CaC14158.1"
/db_xref="GI:10944516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sw:P37072 Sw:P37071 Tr:Q9Y3P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sw:P37070 Tr:Q9QW38 Tr:O77758 Tr:Q9QZ17
Tr:Q9R0K4 Tr:O60412 Tr:Q9QY00 Tr:Q9QW36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        match: ESTs: Em:N68399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Em: AF034896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: cDNAs: Em:Y07557 Em:AF042023
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'note="L1PB1 r
                                                                                                                                                                                                                                                                                                                                                                              6069
                                                                                                                                                                                                                                                                                                                                                                                                'note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="FLAM_C
24448. .24781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="LTR15 repeat: matches 127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LIM4 repeat: matches 5206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"match:
                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Alusg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Alusq repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                 .26391
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                                                                                                                                                                                                                                                                                                                                                                                                                            . 2663
from:
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Em:AF042023 Em:AF091573 Em:AF091574 Em:X89670
Em:AF102540 Em:AF010293 Em:M64388 Em:D12820
                                                                                                                       Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                /x repeat: matches 195.
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                                                                                                                                                                                                                                                                                                                                               repeat:
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  \vdash
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                                                                                                                                                                                                                                            matches 137.
                                                                                                                                                                                                                                                                                                                                               matches 6111.
                                                                                                                                                                                                                                                                                                  matches
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44788
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0
100.000
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Homo sapiens chromosome 6 clone
SEQUENCE, 15 unordered pieces.
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Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:7259782.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Anderson,S., Ballwin,C., Barna, Bastien,Y., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodgo, M., Dowlo, M., Dewar,K., Diaz,J.S.,
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1 (bases 1 to 176277)
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NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 168929 bases at least Q40 Consensus quality: 172827 bases at least Q30 Consensus quality: 174151 bases at least Q30 Insert size: 176000; agarose-fp Insert size: 174877; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L8577
Center clone name: 635_0_11
----- Summary Statistics
                                                                                                                                                Quality coverage: 4.5 in Q20 bases; Quality coverage: 4.6 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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3097: gap of 100 bp
5606: contig of 2509 bp
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70520: gap of 100 bp in

80466: contig of 9946 bp in

10566: gap of 100 bp

93325: contig of 11759 bp in
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131898: contig of 21226 bp in length
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26545: contig of 5806 bp in length
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Ratio: 5.115
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                                                      ThrGlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuPr 167
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             rTyrAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyA
                                                                                                                 TGCTCAAGTTATCTTGTGTTGAGACAACAGCAAATGAGGCTGAACTATTC
                                                                                                                                euLeuLysLeuSerCysValGluThrThrAlaAsnGluAlaGluLeuPhe
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ORGANISM
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Ehlers, A., Beck, S., Forbes, S.A., Trowsdale, J., Volz, A.,
and Ziegler, A.
MHC-linked olfactory receptor loci exhibit polymorphism
contribute to extended HLA/OR-haplotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1074)
2 iegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Ziegler,A., Ehlers,A., Volz,A., Younger,R. and Beck Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck Polymorphic olfactory receptor genes and HLA loci
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                                                                                                                                      Submitted (06-Nov-2000) Ehlers A., Institut fuer Immungenetik, Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berli
                                                                                                                                                                                                                                                                                                                                                                        Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer Lindahl,K., Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J., Volz,A., Ziegler,A. and Beck,S. Characterisation of clustered MHC-linked Olfactory Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Springer-Verlag, Tokyo, Japan (2000)
2 (bases 1 to 1074)
2 iegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Volz,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extended haplotypes
(in) Kasahara,M. (Ed.);
MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6M1-10*02 gene; olfactory receptor
                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphisms in olfactory receptor genes: a cautionary note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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     /db_xref="taxon:9606"
/chromosome="6"
/cell_line="KR3598"
1. .1074
                                                                        /organism="Homo sapiens"
                                                                                                             Location/Qualifiers
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HLA loci constitute
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51 CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT
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IFLALGSTECLLLAVMCFDRFVAICRPLHYSIIMHQRLCFQLAAASWISGFSNSVLQS
TWTLKMPLCGHKEVDHFFCEVPALLKLSCVDTTANEAELFFISVLFLLIPVTLILISY
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FCGIIAPMLNPLIYTLRNKEVKEAFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNF
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/protein_id="CAC20513.1"
/db_xref="GI:12054411"
/translation="MNWVNKSVPQEFILLVFSDQPWLEIPPFVWFLFSYILTIFGNLT
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/codon_start=1
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Forbes, S.A., Horton, R., Milne, S., Mungall, A.J., Tro
Volz, A., Ziegler, A. and Beck, S.
Characterisation of clustered MHC-linked Olfactory
                                                                                          4 (bases 1 to 1074)
Ehlers, A., Beck, S.,
Ehlers, A
                             Unpublished
                                            MHC-linked olfactory receptor loci exhibit polymorphism contribute to extended HLA/OR-haplotypes
                                                                              and Ziegler, A.
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Polymorphisms in olfactory receptor genes: a cautionary note
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2 (bases 1 to 1074)
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Polymorphic olfactory receptor genes and HLA loci constitute
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Ziegler,A., Ehlers,A., Forbes,S.A., Trows
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TWTLKMPLCGHKEVDHFFCEVPALLKLSCVDTTANEAELFFISVLFLLIPVTLILISY
AFIVQAVLRIQSAEGQRKAFGTCGSHLIVVSLFYGTAISMYLQPPSPSSKDRGKMVSL
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/db_xref="taxon:9606"
/chromosome="6"
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/translation="MNWVNKSVPQEFILLVESDQPWLEIPPFVMFLFSYILTIFGNLT
IILVSHVDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICNTRKVISYGGCVAQLF
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/protein_id="CAC20504.1"
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                                                                      Springer-Verlag, Tokyo, Japan (2000)
2 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale
Younger,R.M. and Beck,S.
Polymorphisms in olfactory receptor genes: a
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1074)

Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, j.,

Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S.

Polymorphic olfactory receptor genes and HLA loci constitute
Younger, R.M., Amadou, C., Forbes, S.A., Horton, R., Volz, A., Ziegler, A. and
                                                                                                                                                                                                                                                                                                                                                                                                       HOMO
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(in) Kasahara, M. (Ed.);
                                                           Unpublished
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., Bethel,G.,
, Milne,S., Mu
d Beck,S.
                                                                                                      Forbes, S.A., Trowsdale, J.,
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               Mungall, A.J.,
                            Ehlers, A., Fischer Lindahl, K.,
                                                                                                                                                                    STRUCTURE,
                                                                            cautionary note
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 ACATATGCAACACCAGGAAAGTAATCAGTTATGGTGGCTGTGTGGCCCAG
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Direct Submission
Direct Submission
Submitted (06-NOV-2000) Ehlers
Submitted (105-NOV-2000) Ehlers
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    278
                   **TATAS | atlon="MMWVNKSVPOBFILLVESDOPMLEIPPEVMELESY ILITEGNLI ILVSHVDEKLHTPMYEFLSNLSLLDLCYTTSTVPOMLVIICNTRKVISYGGCVAQLE IFLALGSTECLLLAVMCFDREVAICREPLHYSIIMHQRLCFQLAAASWISGESNSVLOSTTATLKMPLCGHKEVDHEFCEVPALLKLSCVDTTANBAELFFISVLFLLI PVTLILISY AFIVOAVLRIOSAEGRKAFGTCGSHLLIVVSLFYGTA ISMYLQPPSPSSKDRGKMVSLFCIAAPMNLPLIYTLKKEVKEBFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNE FCGIAAPMNPLITTLKKEVKEBFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNE SASCELFVITIENÇNLPORKEP"
                                                                                                                                                                                      /product="olfactory receptor"
/protein_id="CAC20505.1"
/db_xref="GI:12054395"
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/db_xref="taxon:9606"
/chromosome="6"
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Spandauer
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idauer Damm 130, 14050 Berli
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alignment_block: !US-09-755-017-2 x HSA302585 Align seg 1/1 Percent Similarity: Quality: 1319.00 Ratio: 4.517 milarity: 92.994 to: HSA302585 from: Percent L Gaps: Identity: to: 1074 82.484 314

1 MetAsnTrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPh CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS snLeuCysSerIleArgLysValIleSerTyrArgGlyCysValAlaGln 100
||:::|||:: LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA ACTCCTGGACCTTTGCTATACCACAAGTACAGTTCCACAAATGCTGGTAA 250 84 200 67 150 50 100 34

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ACCESSION
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LOCUS HSA302586
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1074)

Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J.,

Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck,S.
             Polymorphic olfactory receptor genes and HLF extended haplotypes
(in) Kasahara,M. (Ed.);
MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION,
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                       Homo sapiens 6M1-10+01 gene for olfactory receptor, aJ302586
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and HLA loci constitute
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               STRUCTURE,
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TOURNAL REFERENCE AUTHORS
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AUTHORS
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Characterisation of clustered MHC-linked Olfactory Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-NOV-2000) Ehlers A., Institut fuer Immungenetik, Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC-linked olfactory receptor loci exhibit polymorphism and contribute to extended {\rm HLA/OR-haplotypes}
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2 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A.,
Younger,R.M. and Beck,S.
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4 (bases 1
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  278
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Milne,S., Mungall,A.J., Trowsdale,J.,
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alignment_block:
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   101
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                                                                       17 eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS
                                                                                                                                  erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg
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CCTATATCTTGACAATCTTTGGCAATCTGACAATAATTCTTGTGTCACAT 150
                                                                                                                   ATGAATTGGGTAAATAAGAGTGTCCCACAGGAGTTCATTCTGTTAGTTTT
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LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe

67

10.75

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KEYWORDS
SOURCE
                                                                              seq_name: gb_pr:HSA302587
                            VERSION
                                       ACCESSION
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|||||||
|ACTGTGTGGTCACAAAGAAGTGGATCACTTCTTCTGTGAAGTCCCTGCTC
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||||||||||||||||||||
|TGCTCAAGTTGTCCTGTGTTGACACAACAGCAAATGAGGCTGAACTATTC
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                                                                                                                                      AACGAAAGGCATTTGGGACATGTGGCTCCCATCTAATTGTGGTGTCACTT
                                                                                                                                                                                                                                                                                                                                                       rgGlnLysAlaPheGlyThrCysGlySerHisLeuIleValValSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGTGCTTTGATAGGTTTGTAGCTATTTGTCGGCCTCTCCATTACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGATTTCAAACTCCACACCCCTATGTACTTTTTCTTAGCAATCTCTC
                                                                                                                                                                                                                                         CAAAGACCGGGGAAAGATGGTTTCTCTCTCTGTGGAATCATTGCACCCA
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                                                                                                                                                                                                                                                                                                                PheTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSe
                                                                                                                                                                                                                                                                                                                                                                                                         TTCATCAGTGTGCTATTCCTTCTAATACCCGTGACACTCATCCTTATATC
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alignment_block:
US-09-755-017-2 x HSA302587
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                                                                                                                  Percent Similarity:
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milarity: 92.994
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Younger, R.M., Amadou, C., Bethel, G., Ehlers, A., Fischer Lindahl, K., Forbes, S.A., Horton, R., Milne, S., Mungall, A.J., Trowsdale, J., Volz, A., Ziegler, A. and Beck, S.
Characterisation of clustered MHC-linked Olfactory Receptor Genes
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Ehlers, A., Beck, S., Forbes, S.A.,
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1 (bases 1 to 1074)
Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J.,
Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck
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ndauer Damm 130, 14050 Berlin,
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                                                                                                                                                              ThrGlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuPr
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                                                                   etLeuAsnProLeuIleTyrThrLeuArgAsnLysGluValLysGluGly
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Direct Submission
Submitted (06-NOV-2000) Ehlers A., Institut fu
Submitted (NOV-2000) Ehlers A., Institut fu
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Ehlers, A., Beck, S.,
and Ziegler, A.
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Characterisation of clustered MHC-linked Olfactory Receptor Genes
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Springer-Verlag, Tokyo, Japan (2000)
2 (bases 1 to 1074)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1074)
Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J.,
Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S.
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AJ302588.1 GI:12054400
6M1-10*01 gene; olfactor
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Younger, R.M. and Beck, S.
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Homo sapiens 6M1-10*01 gene
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FCGIIAPMLNPLIYTLRNKEVKEAFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNF
SASCPIFVITIENYCNLPQRKFP"
                                                                                        /product="01factory receptor"
/protein_id="CAC20508.1"
/db_xref="G1:12054401"
/translation="MUNGYPOLEFILLVESDQPWLEIPPPVMFLFSYILTIFGNLT
IILVSHVDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICMTRKVISYGGCVAQLF
IFLALGSTECLLLAVMCFDRFVAICRPLHYSIIMHQRLCFQLAAASWISGFSNSVLQS
TWTLKMPLCGHKEVDHFFCEVPALLKLSCVDTTANEAELFFISVLFILIPVTLILISY
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/db_xref="taxon:9606"
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Similarity:
                                               PheTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSe
                                                                                                        rgGlnLysAlaPheGlyThrCysGlySerHisLeuIleValValSerLeu
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rLysAspGlnGlyLysMetValSerLeuPheTyrGlyIleIleAlaProM
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                                                                                          AACGAAAGGCATTTGGGACATGTGGCTCCCATCTAATTGTGGTGTCACTT
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receptor,
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MHC-linked olfactory receptor loci exhib
contribute to extended HLA/OR-haplotypes Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer Lindahl,K. Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J., Volz,A., Ziegler,A. and Beck,S.
Characterisation of clustered MHC-linked Olfactory Receptor Genes Springer-Verlag, Tokyo, Japan (2000)
(bases 1 to 1074)
Ziegler, A., Ehlers, A., Forbes, S.A.,
Younger, R.M. and Beck, S. (in) Kasahara,M. (Ed.); MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, FUNCTION: 110-130; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck,S. Direct Submission Submitted (06-NOV-2000) Ehlers Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck,S. Polymorphic olfactory receptor genes and HLA loci constitute Homo sapiens GERMANY Ehlers, A. Unpublished Ehlers, A., Beck, S., Forbes, S.A., Trowsdale, J., Unpublished Polymorphisms in olfactory receptor genes: a Unpublished extended haplotypes 6M1 - 10 * 01Universitaetsklinikum Charite, in Human and Mouse AJ302589.1 GI:12054402 (bases 1 to 1074) (bases 1 to 1074) (bases 1 to 1074) /product="olfactory receptor"
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IFLALGSTECLLLAVMCFDRFVAICRPLHYSIIMHQRLCFQLAAASWISGFSNSVLQS

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alignment_scores:
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                                                                LeuValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIleSe
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FCGIIAPMLNPLIYTLRNKEVKEÞFKRLVAKSLLNQEIRNMQMISFAKDTVLTYLTNF
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Direct Submission
Submitted (06-NOV-2000) Ehlers A.,
Submitted (Nov-2000) Ehlers A.,
Spa
                                                                                                                                                                                                                                   and Ziegler,A.

MHC-linked olfactory receptor loci exhibit contribute to extended HLA/OR-haplotypes
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AJ302590.1 GI:12054404
6M1-10*01 gene; olfactory receptor
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Ehlers, A., Beck, S.,
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Characterisation of clustered MHC-linked Olfactory Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Springer-Verlag, Tokyo 2 (bases 1 to 1074) Ziegler, A., Ehlers, A.,
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1 (bases I to 1074)
2 iegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J.,
Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck
                                                                                                                                                                                                                        Unpublished
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MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION,
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TWTLKMPLCGHKEVDHFFCEVPALLKLESVDTTAMAELFFISVFFLIIJSY
AFIVQAVLRIQSAEGQRKAFGTCGSHLIVVSLFYGTAISMYLQPPSPSSKDRGKMYSL
FCGIIAPMLNPLIYTLRKKEVKBAFKRLVAKSLLNQEIRMQMISFAKDTVLTYLTNF
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/protein_id="CAC20510.1"
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/translation="MNWVNKSVPQEFILLVFSDQPWLEIPPFVMFLFSYILTIFGNLT
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                                                       and Ziegler, A.
MHC-linked olfactory recontribute to extended
                                                                                                                                                                  Forbes, S.A., Horton, R., Milne, S
Volz, A., Ziegler, A. and Beck, S
Characterisation of clustered N
                                                                                                                                                                                                                                                                         Springer-Verlag, Tokyo, Japan (2000)
2 (bases 1 to 1074)
Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J.,
Younger,R.M. and Beck,S.
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Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J
Uchanska-Ziegler,B., Volz,A., Younger,R. and Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens 6M1-10*01 gene
AJ302591
                                                                                                                                                                                                                                                                                                                                                                                Polymorphic olfactory receptor genes and extended haplotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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6M1-10*01 gene; olfactory receptor.
                                          Unpublished
                                                                                                       Ehlers, A., Beck, S.,
                                                                                                                                   Unpublished
                                                                                                                                                                                                              Younger, R.M., Amadou, C.,
                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                           Polymorphisms in olfactory receptor genes: a
                                                                                                                                                       in Human and Mouse
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                                                                                                       Forbes, S.A.,
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ed HLA/OR-haplotypes
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fccgilapwlupliyTlrnkcvkcafkrlvaksllngeirnmomisfakdTvlftvInf
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            Younger, R.M., Amadou, C., Bethel, G., Ehlers, A., I
Forbes, S.A., Horton, R., Milne, S., Mungall, A.J.,
Volz, A., Ziegler, A. and Beck, S.
Characterisation of clustered MHC-linked Olfacto
                                                                                                                              Ziegler, A., Ehlers, A., I
Younger, R.M. and Beck, S
                                                                                                                                                                                                                                              Polymorphic olfactory receptor genes extended haplotypes
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Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J., Uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S.
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AJ302592
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2 (bases 1 to 1074)
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                                                                                                              Polymorphisms in olfactory receptor genes: a
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MHC-linked olfactory receptor loci exhib
contribute to extended HLA/OR-haplotypes
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IILVSHVDFKLHTPMYFFLSNLSLLDLCYTTSTVPQMLVNICOTRKVISYFSUSYDLF
IFLALGSTECLLLAVMCFDRFVAICRFLHYSIIHHQRLCFQLAAASWISGFSNSVLQS
TWTLKMPLCGHKBVDHFFCEVPALLKLSCVDTTANEAELFFISVLFLLIVTLILISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheLysArgLeuValAla.ArgValPheLeuIleLysLys 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rTyrAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyA
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|||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTATGGTACAGCTATCTCCATGTACCTGCAACCACCTTCACCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTCAAGTTGTCCTGTGTTGACACAACAGCAAATGAGGCTGAACTATTC
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                                                                                                                                                                                       HS193B12 100375 bp DNA PRI 23-NOV-1999
HUMAN DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3.
Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j
genes, histone pH2b.i and hypothetical protein A4 pseudogenes,
histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene,
olfactory receptor OL1 like gene, ESTs STSs and predicted CpG
               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 100375)
Wild,A.
                                                                                                                Z98744.1 GI:3080457
6p21.3-22.3; A4; CpG island; Glycine tRNA;
H2A/d; H2B; H2B.2; H2B/d; H3; H3.1; H3.F; F
                                                                                                                                                               islands.
298744
                                                                           Homo sapiens
                                                                                                   olfactory receptor; pH2b
                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                   ; н1.5;
н3/j; н
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                                                                                                                    H4; H4.k; histone;
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FEATURES
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193B12 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed in collaboration by the Sanger Centre chromosome 6 mapping group and Armin Volz & Andreas Ziegler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Apr 24, 1998 this sequence version replaced g1:2578067.
IMPORTANT: This sequence is the entire insert of clone 193B12.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-DEC-1997) Chromosome 6 Project Group (http://www.sanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David Ruddy, Jeffrey Gruen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1001. .1308)
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complement(1589. .>2087)
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W49399 AA396588 AA080125 W41523 AA218213 AA423665 AA562098
AA493023 AA237851 W41584 AA255145 AA327803 AA064568
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GAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1589. .2087)
/gene="H2A/d"
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AA061654 H15508 W41535 AA272868 AA453105 W65215 AA23151
AA073767 AA528953 AA492640 W11262 AA060372 AA027719
AA143419 U90551; match: cDNAs L19778 L19779 X58069 X1485
D17284; match: genomic DNAs Z83739 X83549 Z83736 Z83742
X05862 Y00117 X16148 Z30940 U62674 X57138 U62669 X02218
U62673 X07763 X07758"
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534. .768
                                                                                                                                                                       /note="putative CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1688. .2080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="histone H2A'
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incomplete repeat"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                              [AQGGVLPNIQAVLLPKKTESHHKAKGK"
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/product="histone H2A"
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                                                                                                                                                                                                                                                                                                                                           'protein_id="CAB11417.1"
'db_xref="GI:3080458"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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N42055 N99711 N31296 N31249 W71872 AA255154 N28495
                       /note="AluYb8
20912. .20996
                                                              20574.
                                                                             'note="MLT1B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4365. .4499
/note="AluJo repeat: matches
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /LKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="H2B.1'and H2B.2 like;
P33778 P02278 P02294 Q64477 (
                                                                                                                                            /note="MLT1B repeat: matches 1.
20197. .20490
                                                                                                                                                                                                   /note="MIR repeat: matches 173.
                                                                                                                                                                                                                          /note≖"AluSx repeat: matches 1.
∟9116. .19178
                                                                                                                                                                                                                                                                                     note="2
                                                                                                                                                                                                                                                                                                            18070.
                                                                                                                                                                                                                                                                                                                                                                                                          note="match: BAC end B47865"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSp repeat: matches 1.
15893...16409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     incomplete repeat"
2834. .13127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="22 copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 2.
l1933. .11977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="39 copies of 2 mer 82 % conserved"
7038. .7077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGELAKHAVSEGTKAVTKYTSSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="H2B/d"
/note="H2B.1'and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="H2B/d"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="histone H2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
                                                                                                                                                                                                                                                                                                            'note="match: 5' ESTs D31045 D31402"
.8070. .18215
                                                                                                                                                                                                                                                                                                                                                                note-"Alux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR2 repeat: matches 100. .146 of consensus" .2051. .12094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="20 copies of 2 mer 85 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MPEPSKSAPAPKKGSKKAVTKAQKKDGKKRKRSRKESYSVYVYK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="SPTREMBL:Q99877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="CAB11418.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6723
                                                                                                                                                                                                                                                                                                                                                    .18149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .12640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 copies of 4 mer 80 % conserved'
                                                                                                        20572
                                                                                                                                                                                                                                                                                     copies of 73 mer 95 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                         17463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luSg repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'GI:3080459"
                                                                                                                     repeat: matches 301.
                                                                                                                                                                                                                                                                                                                                                                repeat: matches 293.
  repeat: matches 1.
                                       repeat: matches 308. .1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 mer 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 120.
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                                                                               matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 3.
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7 CE07075
                                                                               84.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 % conserved"
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                                                                                                                                                               .95 of consensus"
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                                                                               .161 of
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                                                                                                                     .8 of consensus*
.85 of consensus"
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alignment_block:
US-09-755-017-2 x HS193B12/rev
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                                                                                                                                 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg
                                                                                       ACTCCTGGACCTTTGCTATACCACAAGTACAGTTCCACAAATGCTGGTAA
                                                                                                                                                                                                                                                                                                                                                                  Quality: 1319.00
Ratio: 4.517
milarity: 92.994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="2 copies of 26 mer 96 % conserved" complement(27803, .28142) /gene="pHZB.i"
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Alusq repeat: <29070. .>29531 /gene="H2A.i"
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27829. .29369
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23759. .24062
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/note="AluSx repeat: matches 1.
28508. 28807
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25062. .25189
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REFERENCE
AUTHORS
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SOURCE
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LOCUS AC024428 1
                                                                                                                                                                         REFERENCE
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                                                                                                                                          AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                     Homo sapiens chromosome
SEQUENCE, 17 unordered p
ACO24428
        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Costle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 166758)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 3, clone RP11-59801
DeArellano,K., Demm.,
Thor.J., Ferreira,P.,
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                        Tandun
                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT
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WORKING DRAFT
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                                                                                                                                                                                        Homo
                                                                                         Allen, N.,
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TITLE JOURNAL COMMENT

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Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7272173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riley, R., Rogov, P., Rothman, D., Roy, A., S
Severy, P., Spencer, B., Stange-Thomann, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 156318 bases at least Q40 consensus quality: 161224 bases at least Q30 consensus quality: 163451 bases at least Q20 Insert size: 191000; agarose-fp Insert size: 165158; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.0 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L69
Center clone name: 598_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center Center code: WIBR
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1446: gap of 12:
7420: contig of 12:
7520:
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18958: contig of 4600 bp
)58: gap of 100 bp
23968: contig of 4910 bp
                                               346: gap of 100 bp
37679: contig of 9033 bp
779: gap of 100 bp
45607: contig of 7828 bp
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Iliev,I., Johnson,R., Jones,C., Kann,L., Kara
54439: contig of 8732
                                                                                                                                                        68: gap of 100 bp 28546: contig of 4478 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: gap of 100 bp
3025: contig of 1900 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025: contig of 1025 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                     120: contig of 2974 bp in length
                                                                                                                                                                                                                                                                                                                       contig of 3489
                                                                                                                                                                                                                                                                                                                                                           100 bp
of 3149 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
                                                                                                                                                                                                                                                                                                                                                   100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
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alignment_block:
                                                                                                                                                                                           alignment_scores:
                                                               Align seg 1/1 to:
                                                                                             US-09-755-017-2 x AC024428
                                                                                                                                            Percent Similarity:
99340 ATGAATTGGGTAAATAAGAGTGTCCCACAGGAGTTCATTCTGTTAGTTTT 99389
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               Quality: 1319.00
Ratio: 4.517
milarity: 92.994
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98660 98759: gap of 100 bp
98760 127843: contig of 29084 bp in length
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                                                               AC024428
                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
98760 .127843
                                                                                                                                                                                                                                                         /note="assembly_fragment"
33823 c 33960 g 48591
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/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                            note="assembly_fragment"
|27944. .166758
                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
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37780. .45607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
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24069. .28546
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166758: contig of 38815 bp in length
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77842: contig of 14012 bp
942: gap of 100 bp
9859: contig of ^^~~
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63730: contig of
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                                                               to: 166758
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eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS
|||||||:::||||:::||
CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT
                                                                                                                                                                                                                                                                             etLeuAsnProLeuIleTyrThrLeuArgAsnLysGluValLysGluGly 300
                                                                                                                                                                                                                             PheTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSe 267.
                                                                                                                                                                                                                                                                                                                                                euLeuLysLeuSerCysValGluThrThrAlaAsnGluAlaGluLeuPhe 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg
                                                                                                                                        CAAAGACCGGGGAAAGATGGTTTCTCTCTCTGTGGAATCATTGCACCCA 100189
                                                                                                                                                                                                             TTTTATGGTACAGCTATCTCCATGTACCTGCAACCACCTTCACCCAGCTC 100139
                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATCAGTGTGCTATTCCTTCTAATACCCGTGACACTCATCCTTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIleSe 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTCAAGTTGTCCTGTTGACACAACAGCAAATGAGGCTGAACTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oLeuCysAspProTyrValIleAspHisPheLeuCysGluValProAlaL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGGCTTTAGCAATTCAGTATTACAGTCCACCTGGACACTTAAGATGCC 99839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTATATCTTGACAATCTTTGGCAATCTGACAATAATTCTTGTGTCACAT
                                                                                                                                                                       rLysAspGlnGlyLysMetValSerLeuPheTyrGlyIleIleAlaProM
                                                                                                                                                                                                                                                                                                                                                                                  rTyrAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGTGTGGTCACAAAGAAGTGGATCACTTCTTCTGTGAAGTCCCTGCTC
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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LOCUS AC025941 1
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Howland,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,Y., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:7259782. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome SEQUENCE, 15 unordered p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
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NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 168929 bases at least Q30 Consensus quality: 172827 bases at least Q30 Consensus quality: 174151 bases at least Q20
                                                                                                                                                                                                                                                            Insert size: 176000; agarose-fp Insert size: 174877; sum-of-contigs Quality coverage: 4.5 in Q20 bases; Quality coverage: 4.6 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L8577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 635_0_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176277 bp
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6 clone RP11-635011 map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100% of reads
                                                                                                                                                                                                                                                                  sum-of-contigs
                                                                                                                                                                                                                                                                                                 agarose-fp
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8 5606: contig of 2
7 5706: gap of 100
7 9209: contig of 3
                                                                                                                                                                                                                                                                                               vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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131999. .176277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-635011"
/clone_lib="RPCI-11 Human
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                                                                          note="assembly_fragment"
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59115: gap of 100 bp
70420: contig of 11305 bp in
70520: gap of 100 bp
80466: contig of 9946 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                note-"assembly_fragment"
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l5. .20639
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176277: contig of 44279 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4808: gap of 100 bp in 183: gap of 10915 bp in 1935 sp in 1959015: contin of 109 bp
                                                                                                                                                                                                                                                                                                                                                                   e-"assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0672: gap of 100 bp
131898: contig of 21226 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425: gap of 100 bp
110572: contig of 18147 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739: gap of 100 bp
26545: contig of 5806 bp in 1
345: gap of 100 bp
37068: contig of 10423 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66: gap of 100 bp
92325: contig of 11759 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13614: contig of 4305 bp in
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.US-09-755-017-2 x AC025941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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             TTCATCAGTGTGCTATTCCTTCTAATACCCGTGACACTCATCCTTATATC
                                                                                                                                                         LeuValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIleSe
                                                                                                                                                                                                                                                                                                 oLeuCysAspProTyrValIleAspHisPheLeuCysGluValProAlaL
                                                                                                                                                                                                                                                                                                                                                      ThrGlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuPr
                                                                                                                                                                                                                                                                                                                                                                                                                 alIleMetHisGlnArgLeuCysLeuGlnLeuAlaAlaAlaAlaSerTrpVal 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snLeuCysSerIleArgLysVall1leSerTyrArgGlyCysValAlaGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ### ACTCCTGGACCTTTGCTATACCACAAGTACAGTTCCACAAATGCTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT
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                                                                                          rTyrAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyA
                                                                                                                                                                                                                                                                                                                                                                                                 TTATCATGCACCAGAGGCTCTGCTTCCAGTTGGCAGCTGCATCCTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGTGCTTTGATAGGTTTGTAGCTATTTGTCGGCCTCTCCATTACTCAA 41471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATATGCAACACCAGGAAAGTAATCAGTTATGGTGGCTGTGTGGCCCAG
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                                                                                                                                                                                                                                                                     ACTGTGTGGTCACAAAGAAGTGGATCACTTCTTCTGTGAAGTCCCTGCTC
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Ratio: 4.517
milarity: 92.994
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FEATURES

source

BASE

COUNT

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234 41771

41721 217 41623 184

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/SIDS2/gcgdata/geneseq/geneseqn/NA2001
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Database sequences: 930621
Database length: 428662619
Search time (sec): 112.140000
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/SIDS2/gcgdata/geneseq/geneseqn/NA2001
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-CAL -OUTFMT=pfs
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-USER=US09755017_@CGN1_1_213 -NCPU=6 -LCPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL-frame+_P2n.model -DEV=xlh
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-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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.DAT:AAH32019
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.DAT:AAC77005
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/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH75755
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                                                                                                The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties
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seq_documentation_block:
ID AASO8541 standard; cl
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AC AASO8541;
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AC AASO8541;
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AC AASO8541;
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DT 26-SEP-2001 (first e
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DNA encoding novel hu
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Human; novel G-protei
KW diagnostic; ss.
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OS Homo sapiens.
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FH Key Locat
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New human G protein-coupled receptor and polynucleotides encoding the receptor, useful in identifying, selecting or validating new molecular targets for drug discovery and in diagnostic or prognostic assays

WPI; 2001-442145/47. P-PSDB; AAU04689.

(LEXI-) LEXICON GENETICS

Wilganowski NL, B, Sands AT;

Turner CA,

Friedrich

é

Abuin

Claim 1; Page 61; 65pp; English.

The sequence represents the coding sequence of novel human G-protein coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful in identifying, selecting or validating novel molecular targets for drug discovery, as well as in diagnostic or prognostic assays. These are also useful in microarrays or other assay formats, for screening collections of genetic material from patients who have a particular medical condition or for identifying mutations associated with a particular disease. 222 A; 228 C; 187 <u>ი</u> 305 T; 0 other; particular medical condition a particular disease.

alignment_scores:

Percent Similarity: Quality: Ratio: 1601.00 5.115 100.000 Length: Gaps: Percent Identity: 100.000

alignment_block: ·US-09-755-017-2 x AAS08541

Align seg 1/1 to: AAS08541 from: 1 .0 942

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                                            etLeuAsnProLeuIleTyrThrLeuArgAsnLysGluValLysGluGly
                                                                                         CAAGGACCAAGGAAAGATGGTTTCTCTCTTCTATGGAATCATTGCACCCA
                                                                                                     rLysAspGlnGlyLysMetValSerLeuPheTyrGlyIleIleAlaProM
                                                                                                                                     TTTTATAGTACAGCCGTCTCTGTGTACCTGCAACCACCTTCGCCCAGCTC
                                                                                                                                                                                 GACAAAAAGCATTTGGGACATGTGGTTCCCATCTAATTGTGGTGTCTCTT
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                                                                                                                                                                                                                                                                        CTTGTCAGTGAGCTCTTCCATCTAATACCCCTGACACTCATCCTTATATC
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seq_documentation_block:
ID AAS08542 standard;
                                                                                    seq_name:
                                                                                 /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS08542
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alignment_block: US-09-755-017-2 x AAS08542

Align seg 1/1 to:

AAS08542

from: 1

to: 1488

198

1 MetAsnTrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPh

ATGAATTGGGTAAATGACAGCATCATACAGGAGTTTATTCTGCTGGGTTT

alignment_scores:

Quality:

1601.00 5.115 100.000

Length: Gaps: Percent Identity:

: 313 : 0 : 100.000

Sequence

1488 BP; 421 A;

333 C;

254

G; 477 T; 3 other;

Ratio: Percent Similarity:

cDNA; 1488

₽P

298

50

34 247

297

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The sequence represents the open reading frame (ORF) encoding novel human 6-protein coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful in identifying, selecting or validating novel molecular targets for drug discovery, as well as in diagnostic or prognostic assays. These are also useful in microarrays or other assay formats, for screening collections of genetic material from patients who have a particular medical condition or for identifying mutations associated with a particular disease.
                                                                                                                                                                  New human G protein-coupled receptor and polynucleotides encoding the receptor, useful in identifying, selecting or validating new molecular targets for drug discovery and in diagnostic or prognostic assays
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P-PSDB; AAU04689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic;
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                                                                                                                                           Disclosure; Page 62-63; 65pp; English.
                                                                                                                                                                                                                                                                               Walke DW,
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                                                                                                                                                                                                                                                                                                      LEXICON GENETICS
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/*tag= a
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/product= "Novel G-protein coupled receptor (NGPCR)"
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seq_name:
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AAH31669 standard;
30-JUL-2001
                            AAH31669;
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Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
                                                                                                                         Human
                                                                                                               olfactory receptor polynucleotide,
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Homo sapiens

WO200127158-A2

06-OCT-2000; 2000WO-US27582

08-OCT-1999; 99US-0158615 24-FEB-2000; 2000US-0184809

(YEDA) YEDA RES & DEV CO

Bellenson J, 2001-290713/30 Smith D, Lancet Ò Glusman e, Fuchs Τ, Yanai

Claim 8; Page 273-274; 1857pp; English.

New polynucleotides which sensation for identifying

encode polypeptides olfactory agonists a

s involved in olfactory and antagonists -

 $\begin{array}{l} \mathbb{Z} \times \mathbb$ scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent figerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals. which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary present sequence is one of a number of isolated polynucleotides

Sequence 1071 вp; 277 Α, 248 <u>ن</u> 201 <u>ი</u> 345 T; 0 other;

alignment_scores:

Percent Similarity: Quality: Ratio: 1319.00 4.517 92.994 Percent Identity: Length: Gaps: 1 82.484

alignment_block: US-09-755-017-2 x AAH31669

Align seg 1/1 to: AAH31669 from: 1 to: 1071

- 1 ATGAATTGGGTAAATAAGAGTGTCCCACAGGAGTTCATTCTGTTAGTTTT
- 17 eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT 34
- 101 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg 150
- 151

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seq_documentation_block:
ID AAH32250 standard; DN
XX
AC AAH32250;
XX
DT 30-JUL-2001 (first &
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DT 30-JUL-2001 reception of the standard of the standard secondary scent determine the standard scent determine the secondary scene determine the seco
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scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                              The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                                                                                                                                                                                                                                                                                                New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
                                of different individuals.
                                                                                                                                                                                                                                                                               Claim 8; Page 508-509; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Bellenson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1999; 99US-0158615
24-FEB-2000; 2000US-0184809
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alignment_block: .US-09-755-017-2 x AAH32250 alignment_scores
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- 151 101 17 34 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg 51 CTCAGATCAACCATGGCTAGAGATTCCACCCTTTGTGATGTTTCTGTTTT LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS CCTATATCTTGACAATCTTTGGCAATCTGACAATAATTCTTGTGTCACAT 67 150 100 50 200 50 34
- 201 67 rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA ACTCCTGGACCTTTGCTATACCACAAGTACAGTTCCACAAATGCTGGTAA 84

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seq_name:
                                                    Human; olfactory receptor; OR; primary scent determination;
secondary scent determination; polypeptide library; odour r
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                                      profile;
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scent fingerprint; scent representation; ds.
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24-FEB-2000; 2000US-0184809
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                               of different individuals.
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alignment_block:
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                                                                  Percent Similarity:
                                                                  Quality: 1138.00
Ratio: 4.138
milarity: 87.859
  AAH32304
from: 1
                                                                  Percent Identity:
to: 939
                                                                                               Length:
                                                                    70.
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1 MetAsnTrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPh ATGAATTGGGAAAATGAGAGCTCCCCAAAAGAGTTTATACTACTTGGCTT 50

eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS

101 34 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg CATACACAATCACCATATTTGGCAATGTGTCCATCATGATGGTGTGCATT

151 51 LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe CTGGATCCCAAACTTCATACTCCCATGTATTTCTTCTCACTAATCTCTC 67

201 rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA 84

disorder; asthma;

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seq_documentation_block:
ID AAC77475 standard; cI
XX
AC AAC77475;
XX
DT 08-FEB-2001 (first 6
XX
DT 08-FEB-2001 reading 1
XX
W Human ORFX ORF3030 pc
XX
W vulnerary; antipsorial
KW anticonvulsant; ostee
KW anticonvulsant; ostee
KW hypotensive; dermatol
KW antiviral; antibactes
KW antiviral; antibactes
KW antianaemic; gene the
KW antianaemic; gene the
KW antianaemic; gene the
KW antianaemic; gene the
KW cardiovascular diseas
KW cholesterol ester sto
                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antifheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
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    cholesterol ester storage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTGAACTCCCTCATCTACAGCCTTAGAAATAAAGATATGAAGGAGGCC
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                                                                                                                                                                                                                                                              polynucleotide sequence SEQ ID NO:6059
                                                                                                                                                                                                                                                                                                                                                                                                          cDNA; 1442
                                                                                                                                                                                                                                                                                                             entry;
    systemic
    lupus erythematosus; infection
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiporvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cosqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; cantiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating conclete cands can be used to express ORFX proteins in gene therapy coectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hyperthematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, callergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coaquiation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 severe combined immunodeficiency; malaria; autoimmune disorder; asthmallergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
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99US-0127728
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.US-09-755-017-2 x AAC77475
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                                                                                                                  Align seg 1/1 to:
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Ratio:
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4.138
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70.607
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Sequence

1442

BP;

378 Α; 319

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268

G; 477

T; 0 other;

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                                                                                       etLeuAsnProLeuIleTyrThrLeuArgAsnLysGluValLysGluGly
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|||||||||:::|||||||||||||:::::::|||
CATACACAATCACCATATTTGGCAATGTGTCCATCATGATGGTGTGCATT
TTCAAGAGGCTGATGCCAAGAATCTTTTTCTGTAAGAAA 1239
                  PheLysArgLeuValAlaArgValPheLeuIleLysLys
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                                                                                                                                                                                                                           PheTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSe
                                                                                                                                                                                                                                                                                                  rgGlnLysAlaPheGlyThrCysGlySerHisLeuIleValValSerLeu
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/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH32231
 101
                    101
                                         51
TTTATGCAGCATCAGGAAAGTAATCAGTTATCGTGGCTGTGTAGCCCAGC
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Percent Identity:

216 0 99.074

alignment_block: US-09-755-017-2 x AAH32231

Align seg 1/1

to:

AAH32231

from:

-

: 0

100 101 50

seq_documentation_block:
ID AAH32231 standard;

DNA; 648 seq_name:

scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds. Claim New polynucleotides which encode polypeptides involved in olsensation for identifying olfactory agonists and antagonists 08-OCT-1999; 99US-0158615 24-FEB-2000; 2000US-0184809 Human olfactory receptor polynucleotide, Sequence of different individuals. Bellenson 06-OCT-2000; 2000WO-US27582 19-APR-2001 WO200127158-A2 30-JUL-2001 (YEDA) YEDA (DIGI-) DIGISCENTS 2001-290713/30 Page 502; 1857pp; 648 BP; ŗ (first entry) RES & DEV CO LTD Smith 144 A; Ď 166 Lancet English. Ç 132 'n G; Glusman 206 SEQ Τ; ი ი 0 other; ID NO: Fuchs T, Yanai olfactory receptors, H

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seq_documentation_block:
ID AAH32025 standard; DN
XX
AC AAH32025;
XX
DT 30-JUL-2001 (first e
XX
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XX
Human olfactory recep
XX
Human; olfactory recep
XX
Human; olfactory recep
XX
Homo sapiens.
XX
Scent profile; scent
XX
PN W0200127158-A2.
XX
PN W0200127158-A2.
XX
PN W0-0CT-2000; 2000WO-L
XX
PP 06-OCT-2000; 2000WO-L
XX
O8-OCT-1999; 99US-C
PR 24-FEB-2000; 2000US-C
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DF 08-OCT-1999; 99US-C
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DF 08-OCT-1999; 99U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
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                                                            Smith D,
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                                                            Lancet D,
                                                            Glusman G,
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                                                            Fuchs T,
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                                                            Yanai I;
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New polynucleotides which encode polypeptides involved in sensation for identifying olfactory agonists and antagonis antagonists olfactory

8, 1857pp; English.

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals. of different individuals.

Sequence 979 BP; 225 A; 260 C; 208 G ; 286 T; 0 other;

alignment_block: US-09-755-017-2 x AAH32025 alignment_scores:
 Quality: Align seg 1/1 Ratio: Percent Similarity: т 6: 954.00 3.614 85.437 from: Gaps: Percent Identity: ш 6 309 2 60.518

1 MetAsnTrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPh eSerAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleS ATGGAAAGAGCTAACGACAGCACCTTCTCTGGATTCATCCTCCTGGGCTT 34

101 TCTACTTTCTGAGCTTTCTGGGCAATGGCACCATTATACTTTTATCCATT 34 erTyrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArg

LeuAspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSe 67

201 TTTTATGGATCTTTGTTTGACCACTTGTACTGTCCCTCAGACACTGGTCA rLeuLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValA 250

301 101 LeuPheIlePheLeuAlaLeuGlyAlaThr.GluTyrLeuLeuLeuAlaV CTATTCATTGCCTTGGGACTCGGGGGGGGGGGGGTGTGTCTTATTGTCTG 350

401 ValIleMetHisGlnArgLeuCysLeuGlnLeuAlaAlaAlaAlaSerTrpVa GTGAGCATCCCCAACTTTGCTTGCAGTTGGTTAACCACTTGGCT 450

451 lThrGlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuP:||||||||:::|||||||:::|||||||CACAGGGTTTGGCAATTCTGTGATACAGACAGCATTGACCATGACTCTCC 167

CCCTCTGTGATAAAAACCAAGTGGATCATTTCTTCTGTGAAGTTCCAGTG roLeuCysAspProTyrVall1LeAspHisPheLeuCysGluValProAla

200

183

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seq_documentation_block:
ID AAH32067 standard; DNA; 927 BE
XX
AC AAH32067;
XX
DT 30-JUL-2001 (first entry)
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DT 30-JUL-2001 (first entry)
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Human olfactory receptor polyr
XX
Human; olfactory receptor; OR;
KW secondary scent determination;
KW scent profile; scent fingerpri
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SCENT PROFILE; SCENT SECONSON S
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                                         New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
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Claim 8; Page 437; 1857pp; English.

these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary of different individuals scents and the identification of the odour receptors used to detect

Sequence 927 BP; 209 Α; 253 C; 176 <u>ი</u> 289 T; 0 other;

alignment_scores:
Quality:
Ratio: alignment_block: US-09-755-017-2 x AAH32067 Percent Similarity: Align seg 1/1 to: 313 363 121 105 263 CAAAGAAGACGATCACTTACGGTGGTGTGTGGCGCAACTCTATATTTCT 113 CCCTTGTGGGAAACTTCACCATAATCATCATCTCATATCTGGATCCCCCT 162 163 13 AATGAGAGTTCCCTAATGGATTTCATCCTTCTAGGCTTCTCAGACCACCC 71 uCysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerI 38 21 oTrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValT თ leArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPheIlePhe 104 LeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLe hrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLys AsnSerValTrpLeuSerThrLeuThrLeuGlnLeuProLeuCysAspPr:::|||:: CACGGCTTTGCCAACAGCTGGCATCTATCTCCTGGCTCAGTGGTTTGGCT lnArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSer TCGGTACATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACC pArgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisG 138 LeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAs CTTCATACCCCAATGTACTTTTTTCTCAGCAACCTCTCTTTACTGGACAT AsnAspSerIleIleGlnGluPheIleLeuLeuGlyPheSerAspArgPr AGTTCCCTAATCCATGCAACTTTTACCTTGCAATTGCCTCTCTGTGGCAA CTGCTTCACTAGCCTTGCTCCTCAGACCTTAGTTAACTTGCAAAGAC AAH32067 944.00 3.688 84.768 from: Percent Identity: \vdash . С Length: 927 302 0 59.603 188 462 154 412 121 88 212 71 54 62

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH32308
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AAH32308 standard;
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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The
                                                       Claim 8; Page 531-532; 1857pp; English.
                                                                                              New polynucleotides which sensation for identifying
                                                                                                                                                         WPI; 2001-290713/30
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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of
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                                                                        euLeuLysLeuSerCysValGluThrThrAlaAsnGluAlaGluLeuPhe
                                                                                                                                                                                                                                                                                                        LeuPheIlePheLeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTATATCTTCACTTTGCTGGGGAACAAAACCATCATTGTATTATCTCAC
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TTTGTCAGTGTCATTATTCTTCTTGTACCTGTTGCATTAATCATATTCTC
                                                                                                                                                 oLeuCysAspProTyrValIleAspHisPheLeuCysGluValProAlaL
                                                                                                                                                                                                               ThrGlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuPr
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                                                          TGCTCAAGCTTGCCTGTTTGACACTACTATGAATGAATCTGAACTCTTC
                                                                                                                       ACTTTGTGGAAGAATAAATTAGAACACTTTCTTTGTGAGGTTCCTCCAT
                                                                                                                                                                                   ATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTGCTTTTAAC
                                                                                                                                                                                                                                              TAGTCATGCACCCTTGTCTGTATGTGCTGATGGCTTCTACTTCATGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAG
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seq_documentation_block:
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secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation; ds.
                                                                                                          The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
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24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human olfactory receptor polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also a scent fingerprint or scent profile), which may be used to re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bellenson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides which encode polypeptides involved in olfactory sation for identifying olfactory agonists and antagonists -
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2000US-0184809.
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TGCCCGGGCTGTACTGAGCATGCAATCAACCACTGGGCTTCAGAAAGTGC

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                                    and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the reand can be used for determining differences in the olfactory factor of different individuals.
                                                              the olfactory faculties
                                                                                     receptors
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Sequence 1011 BP; 217 A; 252 C; 202 G; 340 T; 0 other;

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eValArgAlaValLeuArgIleGlnSerAlaGluGlyArgGlnLysAlaP
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                                                                                                                          erCysValGluThrThrAlaAsnGluAlaGluLeuPheLeuValSerGlu
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                                             ATTTTTGTTCTCATACCTCTCATCCTCATCCTCACTTCCTATGGTGCCAT
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                                                                           LeuPheHisLeuIleProLeuThrLeuIleLeuIleSerTyrAlaPheIl
                                                                                                           CATGTGTTGATACCTAGGCAAATGAGCTGACCCTCATGGTCATGAGCTCC
                                                                                                                                                                       TCGCCTAGTGGATCACTTCTTCTGTGAAGCTCCAGCACTTCTGCGATTAT
                                                                                                                                                                                                                                  ACCTCAGCACTTCATTCCTCCTTTACTTTCTGGATACCCCTATGTAGACA
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                         The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties.
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Quality:
Ratio:
Percent Similarity:
                                                                                                                             these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of a fifference in the olfactory faculties.
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                                                                                                                    different individuals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 oTrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaValSerValTyrLeuGlnProProSerProSerSerLysAspGlnGl
                                                                                                                                                                                                                                                                                                                                                                            LeuPheHisLeuIleProLeuThrLeuIleLeuIleSerTyrAlaPheIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGACGAGTTGACCACTTTCTCTGTGAGATGCCAGCACTAATTGGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oTyrVallleAspHisPheLeuCysGluValProAlaLeuLeuLysLeuS :::|||||||||||::: ::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pArgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaLeuGlyAlaThrGluTyrLeuLeuAlaValMetSerPheAs 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLe
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yLysMetValSerLeuPheTyrGlyIleIleAlaProMetLeuAsnProL
                                                                                                                                                                            heGlyThrCysGlySerHisLeuIleValValSerLeuPheTyrSerThr
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                                                     ATCATATACATGTACCTCCAGCCAGCAAATACTTATTCCCAGGACCAGGG
                                                                                                                                                  TCAACACTTGCAGCTCGCATCTAATTGTTGTCTCTCTCTTCTATGGTACA
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9b_est2: BG19764

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9b_gss: AZ28664867

9b_gss: AZ286625

9b_gss: AZ2911623

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           9b_9ss:AZ392036

9b_9ss:AZ720443

9b_est1:AI148854

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9b_9ss:AZ407823

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gb_htc:AK016338
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-QB-EST -QFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_GOSS -NORM=6X - HEAPSIZE=500
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=6X - HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09755017_eCGN1_1_3653
-NCPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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Compugen Ltd.
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                              Adachi, Aizawa, K. Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Harra, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, F., Toya, T., Yamamura, T., Yasunishi, K., Voshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods in enzymology. 99279253
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                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, Physical and Chemical Research (RIKEN), Labora
                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RIKEN Genome Exploration Research Group Phase
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                              Nature 409, 685-690 (bases 1 to 3063)
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                                                                                                            The Institute of
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6 IM0517B18R MOUSE 1
7 RPCI-24-98II2.TVB
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                   36 hrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAsp
                                                                                                                                                                                                                                                                      3 TrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPheSerAs
                   ThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLe
                                                                                                                                                                                        pArgProTrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrT 36
                                                                                                                                                                                                                                    TGG...AATTCTACCTTGGAAAGTGGATTCATCTTGGTGGGGATTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after selected before cloning and FLC I. Cloning sites, 5' end: SalI; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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/db_xref="GI:1285338"
/db_xref="GI:1285338"
/db_xref="GI:1285338"
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LLLVITVDARLHVPMYLLLRQLSLIDLLETSVVTPNTVVDFLLRDNTISFEGCALQLE
SAMTLGGAEELLLAFWAYDRYVAICHFLUNYMIFMSFKACRLMVAISWILASLSALGHT
VYTMHFPFCWSQEIRHLLGEVPPLKALACADTSQYELMVYVTGVIFLLLPLSAITISV
SLILFTYLHMPSNEGRKKALVTCSSHLTVVGMFYGGATFMYVLPSSFHSPKQDNIISV
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/db_xref="MGD:MGI:1907565"
/db_xref="MGD:MGI:1921647"
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/strain="C57BL/6J"
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Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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                                                   Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sal
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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TGAGTCCAAAGGCCTGCAGGCTCATGGTGGCCATATCATGGATCCTAGCA
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TITLE

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-755-017-2 x AK017036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 TGG...AATTCTACCTTGGAAAGTGGATTCATCTTGGTGGGGATTCTGGA
136 etHisGlnArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGly 152
                                                                                                                                                                        638 TCAGCAATGACATTGGGTGGTGCAGAGGACCTCCTTCTGGCCTTCATGGC
                                                                                                                                                                                                                                                                                                                                                                                            538 TGACCTCCTCTCACATCAGTTGTAACTCCCAACACTGTTGTGGATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 GCCCGGCTTCACGTACCCATGTACCTCCTACTGAGGCAGCTGTCTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 TGTTGGCACTGATCAGCAATGGACTTCTACTCCTGGTCATCACAGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 TGGCAGTGGCTCTCCTGAACTGCTCTGTGCCACAGTTACAACCCTGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 uAspLeuCysTyrThrThrCysThrValProGlnMetLeuValAsnLeuC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 hrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TrpValAsnAspSerIleIleGlnGluPheIleLeuLeuGlyPheSerAs
                                                       CTATGATAGGTATGTGGCCATTTGTCATCCTCTAAACTACATGATCTTCA
                                                                                       rPheAspArgPheValAlaIleCysArgProLeuHisTyrSerValIleM 136
                                                                                                                                                                                                                    IlePheLeuAlaLeuGlyAlaThrGluTyrLeuLeuAlaValMetSe
                                                                                                                                                                                                                                                                                                                 ysSerIleArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="Bab30564.1"
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FYTIVTPALNPLIYSLRNKEVIGAVRRVLGRHILPAHATV"
1 337 c 304 g 398 t
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73.701
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/db_xref="MGD:MGI:1914036"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ∕organism="Mus musculus"
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JOURNAL COMMENT
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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AO077154
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                                                                                                                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ077154
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ077154 479 bp DNA
CIT-HSP-2354D1.TF CIT-HSP Homo
                                                                      Email: mdadams@tigr.org
Clones are available from
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                              Other_GSSs: CIT-HSP-2354D1.TR
                                                                                                                                                                                                                                                                                    Map Building
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                  Use of a random human BAC
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                                                                                                                                                                                                                                                                                                                                                            Venter,J.C.
                                                                 Research Genetics (info@resgen.com).
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORIGIN
                                                                                             seq_documentation_block: LOCUS AZ090606
                                                                                                                            seq_name: gb_gss:AZ090606
                                                                               DEFINITION
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Ratio:
Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                    GSS.
                                                                               AZ090606 692 bp
RPCI-23-27B20.TV RPCI-23
                                                          AZ09060
                                               AZ090606.1 GI:7732649
                                                                      DNA sequence
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                        house mouse.
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4.408
96.296
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2354D1"
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                                                                               genomic clone RPCI-23-27B20,
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alignment_block:
US-09-755-017-2 x AZ090606/rev
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490
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                                                                                                                                                                                                                                                                                                                                                 rGluTyrLeuLeuAlaValMetSerPheAspArgPheValAlaIleC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Similarity:
                                                                                              TIGGCCATCTCCTGGGTGGGAGGCCTTGTGAACTCTCTGACTCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                        TATGCTGGGTGCATGACCCAGTTCTTCATAGCACTCTTACTGGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrArgGlyCysValAlaGlnLeuPheIlePheLeuAlaLeuGlyAlaTh 110
AAGTCTCATCATGACCATACCTCTCTGTGGCCATCAC...CTGAACCACT
                                            rThrLeuThrLeuGlnLeuProLeuCysAspProTyrValIleAspHisP
                                                                                                                                                LeuAlaAlaAlaSerTrpValThrGlyPheSerAsnSerValTrpLeuSe
                                                                                                                                                                                                  GTCGTCCACTACACCACCAGCATTATGCACCCCCTTCTCTGCCATGCA 541
                                                                                                                                                                                                                                                                                                    TGAGTGTGCTCCTTGTGGTGATGGCTTTCGACCGCTATGTCGCTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 27 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Other_GSSs: RPCI-23-27B20.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Fraser, C.M.
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567.50
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81.308
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/clone="RPCI-23-27B20"
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/strain="C57BL/6J"
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                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24.
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BAC
(pdejong@mail.cho.org). Clones may be purchased from BAC
                                                                  (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 367 row: N column: 6
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
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RPCI-24-367N6.TJ RPCI-24
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                          Class: BAC ends
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                                                                                                                BAC end
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/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="RPCI-24-367N6"

/sex="Male"

/clone_lib="RPCI-24"

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alignment_scores:
Quality:
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pletter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library was cloned in the practical cionary versions and bamHl sites using MboI partially digested male C57BL/6J
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2M0241J24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0241J24 R, DNA sequence.
AZ969227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0241 row: J column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Fax: 801 585 7177
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gblraf129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                   polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.
                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0241J24"
                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC2M library"
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Pedersen,T., Reilly
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aGTGTTGTCACACCCATGCTGAATCCTGTAATTTATACG 641
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AZ255734 726 bp DNA GSS 26-JUL-2000 RPCI-23-16619.TU RPCI-23 Mus musculus genomic clone RPCI-23-16619,
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and selected for ampicillin resistance."
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alignment_block:
US-09-755-017-2 x AZ255734
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                                                                                                                                                    42 nLeuThrIleIleLeuValSerArgLeuAspThrLysLeuHisThrProM 59
                                                                                                                                                                                                                                                            26 ProLeuLeuValValPheLeuIleSerTyrThrValThrIlePheGlyAs
CCTCTGTTCTTGTTCCTTGTAATGTATATAGTAACTATGACCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: RPCI-23-16619.TV
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Plate: 166 row: I column: 9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "
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2.973
76.569
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/clone="RPCI-23-16619"
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/strain="C57BL/6J"
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 2 (bases 1 to 1501)
2 (bases 1 to 1501)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Carninci,P., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                Mus musculus (strain:C57BL/6J) adult clone_11b:RIKEN full-length enriched clone:4930580F03.
                                                                                                                 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Loses 1 to 1501)
                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                 AK016338 1501 bp mRNA HTC 05-JUL-2001 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930580F03, full insert sequence.
Konno,H., Okazaki,Y., Muramatsu,M. and Hayash ation and subtraction of cap-trapper-selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721
                                                                                                                                                                                                                                                                     male testis cDNA to mouse cDNA library
                                                                                                                                                                                              Muridae;
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Izawa, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

AL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamorto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and,Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.go.jp/,
Fax:81-45-503-9216)
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Shibata, K., Itoh, M.,
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          398
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BamHI. Host: DH10B
                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="McD:MGI:1909336"
/db_xref="MCD:MGI:1923161"
/tissue_type="testis"
/clone_lib="RIKEN full-length
/dev_stage="adult"
367 c 273 q 463 t
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                          /sex="male"
                                                                                                                                                                      /clone="4930580F03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length mouse
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                                                                          mouse
                                                                      cDNA library"
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-755-017-2 x AK016338
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                                                                                                                                                                                                                                                   1214
                                                                                                                                                                                                                                                                                                                                                     1164
                                                                                                                                                                                                                                                                                                                                                                                                                                               1114 CAAAATTATTCACCAGTTCTTCTGTGATGTCCCCCAGTTGCTCAAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014 CCAGAAAGTGCACTTGGGCTGTGGCAACTGTGTGGCTAAGTGGAGGTATC 1063
                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 LeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAs 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnAspSerIleIleGlnGluPheIleLeuLeuGlyPheSerAspArgPr 21
SerThrAlaValSerValTyrLeuGlnProProSerProSerSerLysAs 269
                                                                                                                                                                                                aPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyArgGlnL 236
                                                                                                                                                                                                                                                   GCAGTTTCCTTTGCCTGT....TTCACTGGGATTGTCATCTCCTATGT
                                                                                                                                                                                                                                                                          oTyrValIleAspHisPheLeuCysGluValProAlaLeuLeuLysLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSer 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pArgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisG 138
||||:::||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCTTTTGCCTGGGGTGAGCTGGCCATTCTCACAGTGATGTCTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uCysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLys 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATATAACCACAATGAGAGGATTCCTCCTCATGGGATTCTCTGACAACCA 664
                                                   AGGTCTTCTACTTGCCTGCCCCATCTTTTTGTTGTCTCATTGTTTCTT 1357
                                                                                              ysAlaPheGlyThrCysGlySerHisLeuIleValValSerLeuPheTyr 252
                                                                                                                                                  CCACATATTCTCCACAGTTCTCAGGATGCCCTCTGCTGAAAGCAGGTCTA 1307
                                                                                                                                                                                                                                                                                                                                                CCTGCTCTAATGACCACCTTGTAATAATGGACATGGTTAGTTTCCTGACT 1213
                                                                                                                                                                                                                                                                                                                                                                                              erCysVal.....GluThrThrAlaAsnGluAlaGluLeuPheLeuVal 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGGAACATTGTACATAACAGGTACACTCTTTATCAGATTCTGTGGGGA 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCTATGTGGCCATCTGCCTCCCATTGCACTATGAGGTCATCATGAGTC 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPheIlePhe 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCATCCCTCTCTCACAGTTCCCCAGTATGTTGACAGTTCCCTGGCAC 863
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BASE COUNT
ORIGIN
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                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AI604386
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Percent Similarity:
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITAGAGITCITGCTCTATCTTTTACACAGTACTACCTCCAACTCTCA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCTGTTATTTATAGTCTGAGAAATGAGACGATAAAG 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vv74c09.xl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1228144 3' similar to SW:OLF2_HUMAN Q15062 OLFACTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 523)
                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was previously sequenced on the data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
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AI604386.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR-LIKE PROTEIN FAT11. ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong
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                           Ratio:
                                                                                                                                                                     149
                                                                                                                                                                     þ
                                                                                                                                                                /tissue_type="whole skin"
/dev_stage="l1 weeks old"
/lab_host="Solf (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: Ecc
/ Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAGTTTTTTTTTTTTTTTTT 3'"
sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
a 133 c 150 g 89 t 2 others
534.00
3.608
86.047
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1228144"
                                                                                                                                                                                                                                                                                                                                                                                                                /sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:4613553
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  Percent Identity:
                                             Length:
172
0
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alignment_block:

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COMMENT
                                                                                                                                                                                                                               REFERENCE
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ORGANISM
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LOCUS AZ913406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_gss:AZ913406
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                                                                                                                                               TITLE
                                                                                                                        JOURNAL
                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 nSerValTrpLeuSerThrLeuThrLeuGlnLeuProLeuCysAspProT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 rgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisGln 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 uAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAspA 122
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                                                  Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                          RPCI-24-165C12.TV RPCI-24 Mus musculus
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 794)
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Medical Center Dr., Rockville,
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301 838 0208
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362 ATTTCTCTTGCTGACACTTCCATTCTGTGGACCCAATGTTCTTGATAC
                                 160 SerThrLeuThrLeuGlnLeuProLeuCysAspProTyrValIleAspHi 176
                                                                                                                                                 143 InLeuAlaAlaAlaSerTrpValThrGlyPheSerAsnSerValTrpLeu
                                                                                                                                                                                                                                                                                                                                                    110 ThrGluTyrLeuLeuLeuAlaValMetSerPheAspArgPheValAlaIl 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 TyrPhePheLeuThrAsnLeuSerLeuLeuAspLeuCysTyrThrThrCy
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                                                                                                                                                                                                                                                                                                     GTGGATGTGTTTTCTCTGTGTGTGATGGCTCTAGATCGATATGTGGCCAT
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254
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/strain="C57BL/6J"
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/clone="RPC1-24-165C12"
/clone_lib="RPC1-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BamH1 sites using MboI partially digested male C57BL/6J DNA."
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ353949 676 bp DNA GSS 02-OCT-
1M0093701F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0093J01 F, DNA sequence.
                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0093 row: J column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Wright, D., Weiss, R.
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quality sequence stop: 676.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0093J01"
                                                            /sex="Male"
                                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Niederhausern, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   2030 E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
    Jackson
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alignment_block:
US-09-755-017-2 x AZ353949
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                                                                                                                                                                                                               402 CATTGGGAAGTTTTGTCATCTTGCTGATCTCATACACAGTCATTCTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 uCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSerAsnSerV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ValAlaIleCysArgProLeuHisTyrSerValIleMetHisGlnArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 alTrpLeuSerThrLeuThrLeuGlnLeuProLeuCysAspProTyrVal 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 euGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAspArgPhe 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ThrThrCysThrValProGlnMetLeuValAsnLeuCysSerIleArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TCCTCAGTAACAGCACCCAAAATGATTGTTGACCTGTTAGTGAAGAAAAA
yArgGlnLysAlaPheGlyThrCysGlySerHisLeuIleValValSerL
                                                                                                                                                                                                                                                                          heLeuValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIle
                                                                                                                                                                                                                                                                                                                                                                                        lGluThr.....ThrAlaAsnGluAlaGluLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCAATAAGATGTTGCTCGGAACATGGATCAGTGGCTTCTTACATTCTA
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                                                                                                                                                SerTyrAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGl
                                                                                                                                                                                                                                                                                                                                      CGACACTTACATTGTTGGTGTTGTTGACAGCCAACAGTGGCACCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTATCCAAGTGGCTCTTGTGGTCCAGCTCCCATTTTGTGGACCAAATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGATCACTATTTCTGTGATGTACATCCTGTACTGAAACTTGCCTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505.50
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alignment_block:
US-09-755-017-2 x AZ909618/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). EAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 222 row: G column: 18
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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RPCI-24-222G18.TJ
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Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeor, Russell, D., de Jong, P. and Fraser, C.M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 797)
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ss: BAC ends.
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2.578
72.556
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/clone="RPCI-24-222G18"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
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seq_name:

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762

RAGE Library Homo

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sequence

DEFINITION ACCESSION

RST12467 Athersys BG193339

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                                                                                 101 TGGAAGGAGATACTCTGATGGGCATCACCTACACAGTCCTCACCCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 erCysValGluThrThrAlaAsnGluAlaGlu.....LeuPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 ATGGGGACAGTGGTGACGACAGCCATTTTCAACCTCACCTTCTGTGGACC
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                                                                                                                         ysAspGlnGlyLysMetValSerLeuPheTyrGlyIleIleAlaProMet
                                                                                                                                                                                                            eTyrSerThrAlaValSerValTyrLeuGlnProProSerProSerSerL
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                                                                                                                                                                                                                              MetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLeuCysTyrThrTh
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                                                                                                                                                                 rCysThrValProGlnMetLeuValAsnLeuCysSerIleArgLysValI
                                                                                                                                                                                                           ATGTACTTCTTCCTCAGCAACATGTCCTTTGTGGACAACTGCTTCTCCAC
                                                                                                                                                                                                                                                                                              ACCTGCTCATCATCCTGGCCATAAGCATAGACTCCCGCCTGCACACCCCC
                                                                                                                                                                                                                                                                                                                                                                             TCTCCTCTTTGTGTTCTTCCTCAGCATGTACCTGGCCACTGTCCTGGGGA 139
                                           TCTCCTTCTCGGCAGTCTCATGCAGATGTATTTTATCAGTGAGCTTGCT
                                                                              leSerTyrArgGlyCysValAlaGlnLeuPheIlePheLeuAlaLeuGly 108
                                                                                                                          C...ACCGTCCCCAAGATGCTGGCCAATCACATACTCAGGACTCAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: scain@athersys.com
High quality sequence stop: 551
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3201 Carnegie Ave, Cleveland, rel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com
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1 (bases 1 to 762)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D.,
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/clone_lib="Athersys RAGE Library"
/cell_line="Hf71080"
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                                                                                                                                                                                                                      University of Utah (University of Utah Rm. 308, Biomedical 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ507393 740 bp DNA GSS 1M0429N15R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0429N15 R, DNA sequence. AZ507393
                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: v
Plate: 0429 row: N column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                        ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GSS.
                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome
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                                                                        High quality sequence stop: 740
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/organism="Mus musculus"
/strain="C57BL/6J"
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                              Genome
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                                                                                                                                                                                                                                                                                                                                                      scaffolding with paired
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alignment_block:
US-09-755-017-2 x AZ607393/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 ValPheLeuIleSerTyrThrValThrIlePheGlyAsnLeuThrIleIl
                                                                                                                                                                                                                                                                                                                                           TGCTGCTGGCAGTGATGGCATTTGATCGATATAAGGCCATTAGTAACCCC
                                                                                                                                                                                                                                                                                                                                                                            euLeuLeuAlaValMetSerPheAspArgPheValAlaIleCysArgPro 129 ::||||||||||| :::|||
                                                   hrLeuGlnLeuProLeuCysAspProTyrValIleAspHisPheLeuCys 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGATGCTTGTAGACCTACTGTCTAAGAATACATCTATTCCTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTTTGATCAGAATGGATCCACAGCTTCACACCACCAATGTACTTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eLeuValSerArgLeuAspThrLysLeuHisThrProMetTyrPhePheL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTTTCTAGTTGTTATCTTACTAATCTGCTGACAAATCTTGGAATGAT
CATTCCACTTATGTTCTGTGGGTCGAATGAGATTAATCATTTCTTCTGT
                                                                                                            aAlaSerTrpValThrGlyPheSerAsnSerValTrpLeuSerThrLeuT
                                                                                                                                                                                                                              CTTTTGTATGCAGTAGACATGTCCAGGAAAGTGTGCTTCCAATTATTGAC
                                                                                                                                                                                                                                                                                 LeuHisTyrSerValIleMetHisGlnArgLeuCysLeuGlnLeuAlaAl 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTGCTATGCAGTTCTTCACTTTCTGTATTTTTATAGATGCTGAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yCysValAlaGlnLeuPheIlePheLeuAlaLeuGlyAlaThrGluTyrL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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74.180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparation someone ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
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//ab_host="E. Coli strain XL10-Gold, T1-resistant, F
//ab_nost="E. Coli strain XL10-Gold, T1-resistant, F
//ab_nost="E. Coli strain XL10-Gold, T1-resistant, F
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/clone="UUGC1M0429N15"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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383

Percent Similarity:

Quality:

Ratio:

490.50 2.666 73.016

Percent Identity:

Gaps:

252 2 42.857

483

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80

96

63

ORIGIN

BASE COUNT

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REFERENCE
AUTHORS
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LOCUS BG197640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 eValValSerLeuPheTyrSerThrAlaValSerValTyrLeuGlnProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 GAGTTCTTATCTCCTACTGTTACATCATCTCATCAGTTCTGAAGATCAGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 GluValProAlaLeuLeuLysLeuSerCysValGluThrThrAlaAsnGl 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 uAlaGluLeuPheLeuValSerGluLeuPheHisLeuIleProLeuThrL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Pel
Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittingt
Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R.,
Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creation of Genome-wide Protein Expression Libraries using Random
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG197640.1
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                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         scain@athersys.com
                                                                                      /note="See 'Creation of Genome-wide Protein Expression / Chibraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

271 c 189 g 220 t 1 others
                                                                                                                                                                                                                                                                  /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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||CATCTGCCACCCCTGCGCTACAACGAGCTCATGAGCCCACGGGGCTGCG 436
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TTCACCCACTCCTTCCTGCTCACCGTCATGGGCTACGACCGCTACGTGGC 386
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ACCTGTTCATGCATGGCCACCGTCTGGAGCGAGCGCAGCCTCCACACGCCC 186
CTGTCA 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerThrLeuThrLeuGlnLeuProLeuCysAspProTyrVallleAs 175
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                                                                                                                                                                                                                          .....CTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGT
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-748-506-7
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US-09-755-017-2 x US-08-748-506-5
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                                                                                                                                                                          122 TCTTAGTATCACTAACAGGAAATACTCTCATAGTCCTTGCTATTTGTACC
                                                                                                                          52 AspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLe 68
                                                                                                                                                                                                                            35 yrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeu 51
                                                                                                                                                                                                                                                                            72 TGAGGTCCCTGGAGAATGCTTCCTCCTGTTCAACCTCATCCTTCTCATGT 121
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                                                                                                                                                                                                                                                   TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/033,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL SPERM RECEPTORS NUMBER OF SEQUENCES: 31
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CITY: Chicago
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                                                                                                                                                                    STRANDEDNESS:
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                                     Quality:
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Two Prudential Plaza, Suite 4900
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                                                                                                                 Sequence 7, Application US/08748506 Patent No. 6159707
                   GENERAL IMFORMATION:
APPLICANT: RONNETT et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
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  CORRESPONDENCE
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ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
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alignment_block:
US-09-755-017-2 x US-08-748-506-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                272
                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                            172 AGTCCATCTCTACACACCCCCATGTACTTCTTCTGGCCAACTTGTCTCT
                                                                                                                                                                                                                                                                                                                                                                           122 TCTTAGTATCACTAACAGGAAATACTCTCATAGCCCTTGCTATTTGTACC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60 FILING DATE: 09-NOV-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                               102 PheIlePheLeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION, DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                 68 uLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValAsnL 85
                                                                                                                                                                                                                                                                                                                                   52 AspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 rAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Pr
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                  35 yrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 TGAGGTCCCTGGAGAATGCTTCCTCCTGTTCACCCTCATCCTTCTCATGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 TGGCAGGAGAATAGTTTGTCTGTCAAACGCTTTGCATTTGCCAAGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TrpValAsnAspSerIle...IleGlnGluPheIleLeuLeuGlyPheSe
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TOTERFAX: 312-616-5700
TOTERFAX: 112-616-5700
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
tSerPheAspArgPheValAlaIleCysArgProLeuHisTyrSerValI 135
                                                                                                                                               TTCTTCTTCATATTCTTTGGTATAACTGAGTGCTGCCTATTGGCAGCCAT
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73.567
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                            TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
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                                                         COUNTRY: U
ZIP: 20005
                                                                                                CITY: WASHINGTON STATE: DC
                                                                                                                                    STREET:
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                                                                                                                                  E: STERNE, KESSLER,
1100 NEW YORK AVE.,
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CAO, LIANG
NI, JIAN
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                             USA
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alignment_block:
US-09-755-017-2 x US-08-467-948A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
                                                                      437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2640
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN REL
CURRENT APPLICATION DATA:
                                                                                                       105
                                                                                                                                         387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 AATCAGACAATGGTCACAGAGTTCCTCCTACTGGGATTTCTCCTGGGCCC 186
   487
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                                                                                                                                                                                                                                                                                                                                                  237 CCCTGCTGGGGAATGGGACCATCCTGGGGCTCATCTCACTGGACTCCAGA 286
                                                                                                                                                                                                                                                                                                                                                                                                                     187 AAGGATTCAGATGCTCCTCTTTGGGCTCTTCTCCCTGTTCTATGTCTTCA 236
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                                                                                                                                                                                                                                                                                                               55
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                                                                                                                                                                                                                                         71 uCysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
CTCCACACCCCCATGTACTTCTTCTCTCACACCTGGCCGTCGTCAACAT
                                                                                                                                                                                                                                                                                               LeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLe
                                                                                                                                                                                                                                                                                                                                                                      hrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                     oTrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValT
                                                                                                   LeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAs 121
                                                                                                                                       CAGCCAAGCCCATCTCCTTTGCTGGTTGCATGACACTAGACTTTCTCTTT
                                                                                                                                                         leArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPheIlePhe 104
                                                                                                                                                                                                          CGCCTATGCCTGCAACACAGTGCCCCAGATGCTGGTGAACCTCCTGCATC
                                                                    TTGAGTTTTGCACATACTGAATGCCTCCTGTTGGTGCTGATGTCCTACGA
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Ratio:
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PATENTIN RELEASE #1.0, VERSION #1.30
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116..1003
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06-JUN-1995
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2.900
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lnArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSer 154
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737

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,94
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR1
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                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                             STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
30-MAR-1995
                                                                                                   US/08/467,947A
                                                                                                                                            VERSION #1.30
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alignment_block:
US-09-755-017-2 x US-08-467-947A-1
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; LOCATION:
US-08-467-947A-1
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pair
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oTyrValIleAspHisPheLeuCysGluValProAlaLeuLeuLysLeuS
                                           CTGGCTATGGTCCATGTGAGCCTCATCCTAAGACTGCCCTTTTGTGGGCC
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                                                                                                                               GGAAAGTCTGCATCACTCTGGGCATCACTTCCTGGACATGTGGCTCCCTC
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; SOFTWARE: Patt
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Rat
US-09-085-371-5
                                                                                                                                                                           alignment_block:
US-09-755-017-2 x US-09-085-371-5
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                                                                                                                                              Align seg 1/1 to: US-09-085-371-5
                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09085371 Patent No. 6218358
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P01511US2 / 09805059
CURRENT APPLICATION NUMBER: US/09/085,371
CURRENT FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: US 08/891,243
PRIOR FILING DATE: 1997-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        887
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                                25 eProLeuLeuValValPheLeuIleSerTyrThrValThrIlePheGlyA 42
                                                                                                        9 IleGlnGluPheIleLeuLeuGlyPheSerAspArgProTrpLeuGluPh
                                                                     GTGAGTGAATTTGTGTTGCTGGGTTTCCCAGCTCCTGCCCCACTGCGAGT
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ACTACTATTTTCCTTTCTCTCTGGACTATGTTTGGTGTTGACTGAAA 127
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                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn
                                                                                                                                                                                                                                       649.00
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76.632
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seq_documentation_block:
 Sequence 1, Application
 Patent No. 5874243
 GENERAL INFORMATION:

US/08827291A

APPLICANT: Macina, APPLICANT: Sathe, TITLE OF INVENTION:

Macina, Robert Sathe, Ganesh

NOVEL OLRCC15 RECEPTOR

Roberto

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-827-291A-1

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                                        euIleTyrThrLeuArgAsnLys 295
                                                                                          CAAGCTGGTCTCTGTACTCTACGCTGTCATTGTACCGTTGTTCAATCCCA
                                                                                                                    yLysMetValSerLeuPheTyrGlyIleIleAlaProMetLeuAsnProL
                                                                                                                                                                                                                                                                                                                                                                                         eValArgAlaValLeuArgIleGlnSerAlaGluGlyArgGlnLysAlaP 238
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                                                                                                                                                                                                                       AlaValSerValTyrLeuGlnProProSerProSerSerLysAspGlnGl
                                                                                                                                                                                                                                                                     TITCAACCTGTGCCTCCCACCTCACTGTTGTGATCATCTTCTATGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                 CACAGGTGCTGATGCGCATCCCCTCAGCTGCTGGCCGCCATAAAGCCT
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TCATCTACTGCTTGCGCAACCAA 900
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alignment_block:
US-09-755-017-2 x US-08-827-291A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFFRENCE/DOCKET NUMBER: GP50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline E
STREET: 709 Swedeland F
CITY: King of Prussia
                                   555 CTGGCAGCAAGTCCATTTCTATGGCTGGTTGTGCCACACAAATTTTCTTC
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
104 PheLeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPh 120
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                                                                                                                                               70 pLeuCysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/827,291A FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                       erIleArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPheIle 103
                                                                                                              CCTCATGCTCATCTGCACCACCGTACCCAAGATGGCCTTCAACTACCTGT
                                                                                                                                                                                      CAGCTCCACACCCCCATGTACCTCCTCCTCAGCCAACTGTCCCTCATGGA
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Ratio:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application Patent No. 6159707
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: RONNett et al.

TITLE OF INVENTION: NOVEL SPERM RECEPTO

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1055
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                ZIP: 60601-6780

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                   STREET: Two Pi
CITY: Chicago
                                                                                                                                                                                                               STATE:
                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pProTyrValIleAspHisPheLeuCysGluValProAlaLeuLeuLysL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCTAAAATTTGTGGACTTATGACTGCCTTTTCCTGGATCCTGGGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08748506
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                                                                                                                                                                                                                                                              Two Prudential Plaza, Suite 4900
                                                                                                                                                                                 SU
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                      Version
                        #1.25
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APPLICATION NUMBER: US/08/748,506 FILING DATE: 08-NOV-1996

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alignment_block:
US-09-755-017-2 x US-08-748-506-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                   102 PheIlePheLeuAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMe 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AGTCCATCTCTACACACCCCCATGTACTTCTTTCTGGCCAACTTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 TCTTAGTATCACTAACAGGAAATGCTCTCATAGCCCTTGCTATTTGTACC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/033,751
                                                                                     152 GlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuProLe 168
                                                                                                                                                                         135 leMetHisGlnArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThr 151
                                                                                                                                                                                                                                                                                                                                                                                              272 TTGTGAGTGAGGCCCGAGAGATCTTTCAGGTGGGATGTGCCACACAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 CCTGGAGATTGGCTATACTTGCTCTGTCATACCCAAGATGCTGCAGAGTC
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l68 uCysAspProTyrValIleAspHisPheLeuCysGluValProAlaLeuL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 uLeuAspLeuCysTyrThrThrCysThrValProGlnMetLeuValAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AspThrLysLeuHisThrProMetTyrPhePheLeuThrAsnLeuSerLe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 yrThrValThrIlePheGlyAsnLeuThrIleIleLeuValSerArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TGAGGTCCCTGGAGAATGCTTCCTCCTGTTCACCCTCATCCTTCTCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TGGCAGGAGAATAGTTTGTCTGTCAAACGTTTTGCCATTTGCCAAGTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-616-5700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 09-NO
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                                             GGATGCATAGTAGGTCTGGGACAGACCAATTTTATTTTCTCCTTGAACTT
                                                                                                                                GAATGAGTCGTGAGGTATGTGCCCACTTGGCAATTGTTTCATGGGTGATG 471
                                                                                                                                                                                                                      GGCCTTTGACCGCTATATGCCTATATGTTCCCCACTCCACTATGCAACCC 421
                                                                                                                                                                                                                                               tSerPheAspArgPheValAlaIleCysArgProLeuHisTyrSerValI 135
                                                                                                                                                                                                                                                                                                          TTTTTCTTCATATTCTTTGGTATAACTGAGTGCTGCCTATTGGCAGCCAT
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   FILING DATE: 08-NOV-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 09-NOV-1S
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ronnett et al. TITLE OF INVENTION: NOVEL SPERM RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772
                     SEQUENCE CHARACTERISTICS:
                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 ACAAAGCCCTTTCAACCTGTTCCTCCCACCTACTTGTAGTCACACTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      672 TGTCAGAATTCTCGTTGCAGTGCTGGTGATGCCTTCACCTGAGGGGGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 rAlaPheTleValArgAlaValLeuArgTleGlnSerAlaGluGlyArgG
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                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Pr
                                                                                 TELEPHONE:
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ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II
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Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SD
                                                           312-616-5700
                                                                                   312-616-5600
                                                                                                                                                                                                                                                                  NUMBER: US/08/748,506
08-NOV-1996
                                                                                                                                                                                     09-NOV-1995
                                                                                                                                                                                                          us 60/033,751
                                            6
                                                                                                                                                                                                                                                                                                                                  Version
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; MOLECULE TYPE: US-08-748-506-6
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US-09-755-017-2 x US-08-748-506-6
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                                                                                                                                                                                                                                                                                                                                 522
                                                                                                                                                                                                                                                                                                                                                           168 uCysAspProTyrVallleAspHisPheLeuCysGluValProAlaLeuL 185
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                                                                                                                                                                                      202 ValSerGluLeuPheHisLeuIleProLeuThrLeuIleLeuIleSerTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 GAATGAGTCGTGAGGTATGTGCCCATTTGGCAATTGTTTCATGGGGAATG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
235 lnLysAlaPheGlyThrCysGlySerHisLeuIleValValSerLeuPhe 251
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                                                                                       rAlaPheIleValArgAlaValLeuArgIleGlnSerAlaGluGlyArgG 235
                                                                                                                                        GCAGCAATCCTCTGTATATCTAGTCCATTTTTGGTGATCCTTTATTCTTA
                                                                                                                                                                                                                                                                             euLysLeuSerCysValGluThrThrAlaAsnGluAlaGluLeuPheLeu
                                                                                                                                                                                                                                                                                                                                 CTGTGGACCTTGTGAGATAGACCACTTCTTCTGTGACCTTCCACCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                        GGATGCATAGTAGGTCTGGGACAGACCAATTTNATTTNCTCCTTGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyPheSerAsnSerValTrpLeuSerThrLeuThrLeuGlnLeuProLe 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tSerPheAspArgPheValAlaIleCysArgProLeuHisTyrSerValI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTTCTTCACATTTTTTGGCATAACTGAGTGCTGCCTATTGGCAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euCysSerIleArgLysValIleSerTyrArgGlyCysValAlaGlnLeu 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rAspArgProTrpLeuGluPheProLeuLeuValValPheLeuIleSerT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCAGGAGAATAGTTTGTCTGTCAAACGCTTTGCATTTGCCAAGTTCTC
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                                           TGTCAGAATTCTCGTTGCAGTGCTGGTGATGCCTTCACCTGAGGGGGCGCC
                                                                                                                                                                                                                                    TGGCACTTGCCTGTGGTGATACATCCCAAAACGAGGCTGCCATCTTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTGAGTGAGGCCAGAGAGATCTCTAGGGAGGGATGTGCCACACAGATG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGGTCCCTGGAGAATGCTTCCTCCTGTTCACCCTCATCCTTCTCATGT
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seq_documentation_block:
; Sequence 9, Application US/08748506
; Patent No. 6159707
alignment_block:
US-09-755-017-2 x US-08-748-506-9
                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                             ; MOLECULE TYPE: US-08-748-506-9 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-748-506-9
                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                       TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ronnett et al. TITLE OF INVENTION: NOVEL NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    922 AGAAGA 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 08-NOV CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two FI
                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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STREET: Two Prudential Plaza, Suite 4900
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                                                                            Ratio:
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N: 435
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72.100
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                                                              Percent Identity:
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Align seg 1/1

to: US-08-748-506-9

from:

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242 GlySerHisLeuIleValValSerLeuPheTyrSerThrAlaValSerVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 spHisPheLeuCysGluValProAlaLeuLeuLysLeuSerCysValGlu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 TCCAGTTGTGATGCTTTCCAAGACATTTTACTGTGGTCCAAACATTATTC
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                                                         842 CTCTTGTGAACATGGTTGTGACACCCCTTCTGAACCCTGTCATCTACACC
                                                                                                          275 erLeuPheTyrGlyIleIleAlaProMetLeuAsnProLeuIleTyrThr 291
                                                                                                                                                                    792 ATACCTGAAGCCAAAGCAGAGAAGCAGAGTGGACACCAACAGAGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                         692 TAGTGAGACTCCCTTCAGCCAGGGAGCGACAGAGAGCTTTTTCCACCTGC
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alignment_block:
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; Sequence 2, Applicatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-988-876-2
Align seg 1/1
                               US-09-755-017-2 x US-08-988-876-2
                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN CO
TITLE OF INVENTION: WITH IMMUNE
                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: PROSNOT01
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 lPheLeu 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                                                            LIBRARY: PROS
CLONE: 364702
                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/08988876 6063596 .
                                                                                                                                                                                                                                                                 : 1828 base pairs
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Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                          linear
 US-08-988-876-2
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                                                                              Percent Identity:
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814 TTCCTCCTAGAAGTCTCAGGGGATCCAGAACTGCAGCCAGTCCTTGC

863

12 PheIleLeuLeuGlyPheSerAspArgProTrpLeuGluPheProLeuLe 28

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seq_documentation_block:
                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-465-980-1
Sequence 1, Application US/08465980 Patent No. 5756309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1164 GTCACCCGCTATATCATTCACC.ATCATGAACCCGTGTTTCTGTGCCTTT 1212
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                                                                                                                                                                                    GAGAAACAGGGATATGAAAAGTGTCCTGCGGCGG
                                                                                                                                                                                                                                       uArgAsnLysGluValLysGluGlyPheLysArg 303
                                                                                                                                                                                                                                                                                                         GTGATGTACACGGTGGTCACCCCCATGCTGAACCCCCTTCATGTACAGCCT 1640
                                                                                                                                                                                                                                                                                                                                         LeuPheTyrGlyIleIleAlaProMetLeuAsnProLeuIleTyrThrLe 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eProLeuThrLeuIleLeuIleSerTyrAlaPheIleValArgAlaValL 226
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alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FETATO, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
                                                                                                                                       434
                                                                                                                                                                                                                                                                          346 TGGGTTGGCTTCCCCCTCCTTTCCATG......TATGTAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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534 TTCCCGAGAGATTAGCATTGAGGCCTGTCTTACCCAGATGTTCTTTATTC 583
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NAME: Ferraro, Gregory D
                                                                                                                                                                                                         384 AATGTGTGGAAACTGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                             22 TrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValTh
                                                                                                                                                                                                                                           38 rIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLysL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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CITY: Roseland
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LOCATION: 274..1233
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                            eArgLysValIleSerTyrArgGlyCysValAlaGlnLeuPheIlePheL 105
                                                                                                                                     TGCACGCTCCGATGTACCTCTTTCTCTGCATGCTTGCAGCCATTGACCTG
                                                                   GCCTTATCCACATCCACCATGCCTAAGATCCTTGCCCTTTTCTGGTTTGA 533
                                                                                                                                                                       euHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLeu
                                                                                                    CysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerIl
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STUART & OLSTEIN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 laValSerValTyrLeuGlnProProSerProSerSerLysAspGlnGly 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 ValArgAlaValLeuArgIleGlnSerAlaGluGlyArgGlnLysAlaPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 euPheHisLeuIleProLeuThrLeuIleLeuIleSerTyrAlaPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 CTATGCAGACACTTTGCCCCAATGTGGTATATGGTCTTACTGCCATTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 rCysValGluThrThrAlaAsnGluAlaGluLeuPheLeuValSerGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784 AATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAAGTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                          CITY: Roseland
STATE: New Jersey
                                                                                                                      COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAGTAACAGCCCAGATTGGCATCGTGGCTGTGGTCCGCGGATCCCTCT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nProLeuIleTyrThrLeuArgAsnLysGluValLys 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eGlyThrCysGlySerHisLeuIleValValSerLeuPheTyrSerThrA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrValIleAspHisPheLeuCysGluValProAlaLeuLeuLysLeuSe
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                                                                                                                                                                                                                                                                                                                                                                                                               Rosen, Craig A. Ruben, Steven M.
                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soppet, Daniel R.
Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
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alignment_block:
US-09-755-017-2 x US-09-053-303-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 TGGGTTGGCTTCCCCCTTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
    155
                                                                                                                                                                                                                               584 ATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGAC
                                                                                                                                                                                                                                                                                                                       534 TTCCCGAGAGATTAGCATTGAGGCCTGTCTTACCCAGATGTTCTTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                               484 GCCTTATCCACATCCACCATGCCTAAGATCCTTGCCCTTTTCTGGTTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 CysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 euHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 rIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 TrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1474 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,134 REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferraro, Gregory REGISTRATION NUMBER: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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snSerValTrpLeuSerThrLeuThrLeuGlnLeuProLeuCysAspPro 171
                                               TACAGTAACAGCCCAGATTGGCATCGTGGCTGTGGTCCGCGGATCCCTCT 733
                                                                                                                                                                               ArgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisGl 138
                                                                                                                                                                                                                                                                       euAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAsp 121
                                                                                     nArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSerA 155
                                                                                                                                     CGTTATGTGGCCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAA
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TTTTTTTCCCACTGCCTCTGCTGATCAAGCGGCCTGGCCCTTCTGCCACTCC 783

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seq_documentation_block:
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                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 nProLeuIleTyrThrLeuArgAsnLysGluValLys 298
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1134 TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGA 1170
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                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
SEQUENCE CHARACTERISTICS:
                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8 . CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 LysMetValSerLeu....PheTyrGlyIleIleAlaProMetLeuAs 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                             NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 Becker Farm Road
                                              201-994-1744
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Ruben, Steven M.
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Li, Yi
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seq_name:

238

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alignment_block:
US-09-755-017-2 x PCT-US95-07093-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: PCT-US95-07093-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                       222 ValArgAlaValLeuArgIleGlnSerAlaGluGlyArgGlnLysAlaPh 238
                                                                                          884
                                                                                                                                                                                                                                                                                                                                                                         734
                                                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 TTCCCGAGAGATTAGCATTGAGGCCTGTCTTACCCAGATGTTCTTTATTC 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 TGGGTTGGCTTCCCCCTCCTTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 nArgLeuCysLeuGlnLeuAlaAlaAlaSerTrpValThrGlyPheSerA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 ATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AATGTGTGGAAACTGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 GCCTTATCCACATCCACCATGCCTAAGATCCTTGCCCTTTTCTGGTTTGA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 euHisThrProMetTyrPhePheLeuThrAsnLeuSerLeuLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 rIlePheGlyAsnLeuThrIleIleLeuValSerArgLeuAspThrLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 TrpLeuGluPheProLeuLeuValValPheLeuIleSerTyrThrValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1474 base pairs
ATACGAACGGTTCTGCAACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTT
                                                                                                                                                                                   CTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGC
                                                                                                                                                                                                                              rCysValGluThrThrAlaAsnGluAlaGluLeuPheLeuValSerGluL
                                                                                                                                                                                                                                                                                                                         TyrValIleAspHisPheLeuCysGluValProAlaLeuLeuLysLeuSe 188
                                                                                                                                                                                                                                                                                                                                                                                                                    snSerValTrpLeuSerThrLeuThrLeuGlnLeuProLeuCysAspPro 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTATGTGGCCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgPheValAlaIleCysArgProLeuHisTyrSerValIleMetHisG1 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euAlaLeuGlyAlaThrGluTyrLeuLeuLeuAlaValMetSerPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysTyrThrThrCysThrValProGlnMetLeuValAsnLeuCysSerIl 88
                                                                                                                                   euPheHisLeuIleProLeuThrLeuIleLeuIleSerTyrAlaPheIle
                                                                                                                                                                                                                                                                            AATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAAGTTGGC
                                                                                                                                                                                                                                                                                                                                                                         TTTTTTTCCCACTGCCTGTGATCAAGCGGCTGGCCTTCTGCCACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAGTAACAGCCCAGATTGGCATCGTGGCTGTGGTCCGCGGATCCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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274..1233
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2.163
63.799
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alignment_block:
US-09-755-017-2 x US-08-599-252-84/rev
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; TOPOLOGY: lir
US-08-599-252-84
                                                                                                                                                       alignment_scores:
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Align seg 1/1 to reverse of: US-08-599-252-84
                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 LysMetValSerLeu.....PheTyrGlyIleIleAlaProMetLeuAs 286
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/OFILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCGTGTTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laValSerValTyrLeuGlnProProSerProSerSerLysAspGlnGly 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGlyThrCysGlySerHisLeuIleValValSerLeuPheTyrSerThrA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nProLeuIleTyrThrLeuArgAsnLysGluValLys 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGA 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAACCTGTGTCACACATTGGTGTGGTACTCGCCTTCTATGTGCCAC 1033
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                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20006-1888
                                                                                                                                                                                                                                                                : 1320 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: MORRISON & FOERSTER 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIMMEL, BRUCE E. THOMAS, WINSTON J. WOLFF, ROGER K.
                                                                                                                                                                                                                                                                                                                                                                       (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRAYNA, DENNIS T
                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                         (202) 887-1500
                                                                                            227.00
3.721
89.706
                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                              29,959
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                                                                                            Percent Identity:
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                                                                                                                                     Length:
                                                                                            68
0
60.294
from: 1
to: 1320
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alignment_scores:
                                                                                                               US-08-436-074-57
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     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,074
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                       TYPE:
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CITY: Washington
                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        NAME: MURASHIGE, KATE REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTTACCCTTTTCTACACAATTGTCACTCCCAGTGTTAACCCCCCTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACATGTACCTCCAGCCAGCAAATACTTATTCCCAGGACCAGGGCAAGT 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20006-1888
                                        Quality:
                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                 90-4030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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VENTION: METHOD TO DIAGNOSE HEREDITARY
                                                                                                                                                                                                                                                                    (202)
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KIMMEL, BRUCE E.
THOMAS, WINSTON J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRAYNA, DENNIS T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORRISON & FOERSTER
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   227.00
3.721
89.706
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                                                                                                                                                                                                                                                                                                                                        29,959
Length: 68
Gaps: 0
Percent Identity: 60.294
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